

pharmaceutical composition to the interior of the cell. The composition and method are used for the introduction of exogenous genetic material into target host cells expressing SECR on their surface. The nucleic acid may encode a functional wild-type or mutant gene or may be an antisense sequence or other nucleic acid having a therapeutic effect. The fusion protein may comprise a protein portion having therapeutic properties, e.g. enzymatic activity, cytokine activity and antibiotic activity which is delivered to a cell surface via the SECR binding moiety. The nucleic acid can be compacted at high concentrations with the carrier molecule at a critical salt concentration. The condensation of such complexes provides structural features to the DNA/cationic lipid complex that prolong in vivo expression.

Query Match 83.5%; Score 517; DB 19; Length 301;
Best Local Similarity 81.0%; Pred. No. 6.3e-38;
Matches 98; Conservative 8; Mismatches 9; Indels 6; Gaps 1;
1 EVQLQSGPELVKPGTSTSRISCKTSYTFTEYTHHWKQSHGKSLWIGINPNNGGTTY 60
127 EVQLQSGPELVKPGASVKISCKTSGYTFTEYTHHWKQSHGKSLWIGINPNNGGTSY 186
61 NQKFKDKATLVDRKSSSTAYMELSLTSDSAVYCAAGWNE-----DYWGQGTTLTVS 114
187 NQKFKDKATLVDRKSSSTAYMELSLTSDSAVYCAAGWNE-----DYWGQGTTLTVS 114
115 S 115
247 S 247

RESULT 8
AAR12356
ID AAR12356 standard; Protein; 141 AA.

AC AAR12356;
DT 15-AUG-1991 (first entry)
DE Heavy chain variable region of murine 2G12 immunoglobulin.
KW Chimeric antibodies; immunoconjugates; HIV; AIDS.
OS Mus musculus.
PN WO9107493-A.
30-MAY-1991.

PF 13-NOV-1990; 90WO-US06615.
PR 13-NOV-1989; 89US-0433730.
PA (XOMA-) XOMA CORP.
PA (GREG) GREEN CROSS CORP.

PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
DR WPI: 1991-178044/24.
DR N-PSDB; AAQ12058.
PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV-1 antigen from sample
PS Disclosure; fig 7; 107pp; English.

CC This is the heavy-chain variable (V) region of a mouse monoclonal antibody (MAB), 2G12, and is specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAB comprising heavy and light chains having murine V regions and human C regions. The chimeric MABs are more effective than murine MAB 2G12 since they have an increased compatibility in humans. The heavy and

CC light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MABs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV.
CC See also AAQ12056-57 and AAQ12059-63.
SQ Sequence 141 AA;

Query Match 83.4%; Score 516.5; DB 12; Length 141;
Best Local Similarity 80.3%; Pred. No. 3.1e-38;
Matches 98; Conservative 8; Mismatches 9; Indels 7; Gaps 1;

OY 1 EVQLQSGPELVKPGTSTSRISCKTSYTFTEYTHHWKQSHGKSLWIGINPNNGGTTY 60
DB 20 EVQLQSGPELVKPGASVKISCKTSGYTFTEYTHHWKQSHGKSLWIGINPNNGGTTY 79
OY 61 NQKFKDKATLVDRKSSSTAYMELSLTSDSAVYCAAGWNE-----FYWGQGTTLTV 113
DB 80 NQKFKDKATLVDRKSSSTAYMELSLTSDSAVYCAAGWNE-----FYWGQGTTLTV 139
OY 114 S 115
DB 140 SA 141

RESULT 9
AAR12234
ID AAR12234 standard; Protein; 140 AA.

AC AAR12234;
DT 19-AUG-1991 (first entry)
DE Mouse MAB 2G12 H chain V region.
KW HIV-1; chimera.
OS Mus sp.
PN WO9107494-A.
30-MAY-1991.
PF 13-NOV-1990; 90WO-US06627.
PR 13-NOV-1989; 89US-0433703.

PA (XOMA-) XOMA CORP.
PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
DR WPI: 1991-178106/24.
DR N-PSDB; AAQ12014.
XX New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
PS Disclosure; Fig 7; 108pp; English.

CC The mouse VH gene product may be used to produce chimeric mouse-human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system.

SQ Sequence 140 AA;

Query Match ~ 83.3%; Score 515.5; DB 12; Length 140;
Best Local Similarity 81.0%; Pred. No. 3.7e-38;
Matches 98; Conservative 7; Mismatches 9; Indels 7; Gaps 1;

OY 1 EVQLQSGPELVKPGTSTSRISCKTSYTFTEYTHHWKQSHGKSLWIGINPNNGGTTY 60
|||||

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:11:26 ; Search time 51.8018 Seconds
(without alignments)
295.816 Million cell updates/sec

Title: US-09-929-546-8

Perfect score: 619

Sequence: 1 EVLQSQGPVLPKPTSVRI.....CAAGNFDYWGQGTITVSS 115

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	619	100.0	115	19	AAW47084
2	619	100.0	115	21	AAW47084
3	619	100.0	115	22	AAW47084
4	619	100.0	130	19	AAW47083
5	619	100.0	130	21	AAW47083
6	619	100.0	130	22	AAW47083
7	517	83.5	301	19	AAW47085
8	516.5	83.4	141	12	AAW47085
9	515.5	83.3	140	12	AAW47085
10	507.5	82.0	118	15	AAW47085

11	507.5	82.0	118	15	AAW60301
12	505.5	81.7	137	17	AAW03724
13	502	81.1	109	22	AAU08980
14	500.5	80.9	110	22	AAU08979
15	497.5	80.4	116	19	AAW71882
16	497.5	80.4	116	21	AAW71882
17	497.5	80.4	118	20	AAW52755
18	497.5	80.4	118	20	AAW52756
19	497.5	80.4	130	19	AAW71886
20	497.5	80.4	135	19	AAW60866
21	497.5	80.4	135	21	AAW80293
22	497.5	80.4	590	18	AAW31751
23	497.5	80.4	590	19	AAW71888
24	497.5	80.4	590	21	AAW12908
25	496	80.1	136	17	AAW06446
26	495.5	80.0	116	19	AAW60864
27	494.5	79.9	120	22	AAW83158
28	494.5	79.9	139	14	AAW38259
29	494.5	79.9	139	15	AAW53288
30	494.5	79.9	139	20	AAW28384
31	494.5	79.9	139	20	AAW28356
32	494.5	79.9	233	14	AAW41710
33	494.5	79.9	235	14	AAW41682
34	494.5	79.9	235	14	AAW41707
35	494.5	79.9	235	14	AAW41715
36	493.5	79.6	116	22	AAW69671
37	492.5	79.6	135	20	AAW68548
38	492.5	79.6	135	22	AAW69682
39	492.5	79.6	135	22	AAW69682
40	492	79.5	118	22	AAW12045
41	491.5	79.4	143	20	AAW50155
42	491.5	79.4	472	20	AAW50157
43	491	79.3	121	13	AAW25408
44	490.5	79.2	240	18	AAW25784
45	490.5	79.2	454	14	AAW30774

ALIGNMENTS

RESULT 1

AAW47084

ID AAW47084 standard; Protein: 115 AA.

XX

AC AAW47084;

XX

DT 26-JUN-1998 (first entry)

XX

DE Mouse J591 monoclonal antibody heavy chain variable region.

XX

DE Mouse; monoclonal antibody; J591; prostate specific membrane antigen;

XX

KW cancer; vascular endothelial cell; metastatic adenocarcinoma.

XX

OS Mus sp.

XX

PN WO9803873-A1.

XX

PD 29-JAN-1998.

XX

PF 17-JUL-1997; 97WO-US12035.

XX

PR 09-APR-1997; 97US-0838682.

XX

PR 18-JUL-1996; 96US-0022125.

XX

XX (CORR) CORNELL RES FOUND INC.

PA

PA Bander NH;

XX

XX WPI; 1998-120937/11.

DR

DR N-PSDB; AAV13950.

XX

PT Destroying cancer cells with agent that binds to prostate specific

PT membrane antigen - on vascular endothelial cells near the cancer, or

on normal, hypertrophic or cancerous prostatic cells, also used for diagnosis

Example 12; Page 55-56; 94pp: English.

The present sequence represents the mouse J591 monoclonal antibody heavy chain variable region from an example of the present invention. The present invention describes the elimination of cancer cells by treating vascular endothelial cells (VEC) close to the cancer with an agent (A) able to bind to the extracellular domain (ECD) of prostate specific membrane antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells. Also described are: (1) the detection of cancer tissue by detecting binding of labelled (A) to VEC close to, or within, a cancer tissue; (2) eliminating or detecting normal, benignly hyperplastic or cancerous prostate epithelial cells using optionally labelled (A); (3) hybridomas that produce a monoclonal antibody (MAb) that binds to PSMA. The method is used to treat renal, urothelial, colon, lung, rectal or breast cancers and metastatic adenocarcinoma of the liver. The diagnostic method is particularly used to detect recurrence of prostatic disease or to monitor the effect of treatments for prostate cancer (presence of PSMA in the serum indicates that prostate cells are being lysed). (A) binds to an epitope of PSMA expressed on live cells (contrast antibody 7E11 which only binds after cell lysis), allowing targeting of live, unfixed cells and thus providing more efficient treatment and diagnosis. Both cancer cells themselves and the VEC on which they depend are killed. All VEC close to cancer cells express PSMA, whatever the type of cancer, but normal VEC do not.

Sequence 115 AA:

XX	Antibody specific for extracellular prostate-specific membrane antigen, useful for diagnosis and treatment of prostate cancer	Example 12; Column 21; 33pp; English.
XX	This sequence is a fragment of the heavy chain of the monoclonal antibody J591. The invention relates to an isolated antibody or its antigen binding portion (I) which binds to an extracellular domain of prostate specific membrane antigen and which does not require cell lysis to bind to the extracellular domain. The antibody or its antigen binding portion is selected for its ability to bind to live cells. (I) is useful for diagnosis of diseases associated with the presence of normal, benign hyperplastic, and cancerous epithelial cells or portions. Also it can be used for identifying the recurrence of such diseases, particularly when the disease is localised in a particular biological material of the patient for e.g. recurrence of prostatic disease. They can also be used alone or bound to a substance effective to kill cancerous prostate epithelial cells as a therapy for prostate cancer. Binding and internalising of the antibody with the prostate specific membrane antigen, permits the therapeutic use of intracellularly acting cytotoxic agents. (I) targets only prostate epithelial cells and other tissue are spared which provides safer treatment particularly for elderly patients. The antibodies bind to living prostate cells and treatments using these antibodies are more effective than those which target lysed prostate cells.	
XX	Sequence 115 AA;	
XX	Query Match 100.0%; Score 619; DB 21; Length 115;	
XX	Best Local Similarity 100.0%; Pred. No. 2.2e-47;	
XX	Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 EVLOQSGPELVKPGTSVRISCKTSGYTFEYTIHWVKQSHGSKLEWIGNINPNNGGTTY 60	
Db	1 EVLOQSGPELVKPGTSVRISCKTSGYTFEYTIHWVKQSHGSKLEWIGNINPNNGGTTY 60	
QY	61 NQFEDKATLTVDKSSSTAYMELRSLTSEDVAVYCAAGNFDYWGQGTTLTVSS 115	
Db	61 NQFEDKATLTVDKSSSTAYMELRSLTSEDVAVYCAAGNFDYWGQGTTLTVSS 115	
RESULT 3		
AAB36221	ID	AAB36221 standard; Protein; 115 AA.
XX	AC	AAB36221;
XX	AC	
XX	AC	
DT	15-FEB-2001	(first entry)
XX		Murine heavy chain monoclonal antibody J591 V region.
XX		Mouse; antibody; heavy chain; prostate cancer; biological agent.
KW		
XX		
OS		Mus sp.
XX		
XX	US6136311-A.	
PN	24-OCT-2000.	
XX		
XX	17-JUL-1997;	97US-0895914.
PF		
XX	06-MAY-1996;	96US-0016976.
PR	18-JUL-1996;	96US-002125.
PR	05-APR-1997;	97US-0838682.
XX		
XX	(CORR) CORNELL RES FOUND INC.	
PA		
PI	Bander NH;	
XX		
XX	WPI; 2001-040234/05.	
DR	N-PSDB; AAC66540.	
XX		

PT Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating
 PT or killing cancerous, especially non-prostate, cells (e.g. breast
 PT cancerous cells or cancerous cells of metastatic adenocarcinoma to the
 PT liver)

XX Example 12; Column 24; 35pp; English.

XX The present invention describes a method of killing cancer cells,
 CC particularly prostate cancer cells, by directing a biological agent to
 CC the cells which then binds to a prostate specific membrane antigen and
 CC causes the molecule to be internalised. The internalisation of the agent,
 CC which may be bound to a drug or which may act to kill the cell alone,
 CC then leads to the death of the cell. The present sequence forms
 CC part of an antibody which may be used as the biological agent of the
 CC invention. In addition to prostate cancer, the method can be used with
 CC renal, urothelial, colon, renal, lung and breast cancer cells, and
 CC cancerous cells of metastatic adenocarcinoma to the liver.

XX Sequence 115 AA;

Query Match 100.0%; Score 619; DB 22; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2.2e-47;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLQSGPELVKPGTSTSRISCKTSGYTFEYTIHWYKQSHGKSLWIGNINPNNGGTTY 60
 Db 1 EVQLQSGPELVKPGTSTSRISCKTSGYTFEYTIHWYKQSHGKSLWIGNINPNNGGTTY 60
 Qy 61 NQFEDKATLTVDKSSSTAYMELSLTSEDSAVYCAAGNFDYWGOGTTLTVSS 115
 Db 61 NQFEDKATLTVDKSSSTAYMELSLTSEDSAVYCAAGNFDYWGOGTTLTVSS 115

RESULT 4

AAW47083
 ID AAW47083 standard; Protein; 130 AA.

XX AC AAW47083;

XX DT 26-JUN-1998 (first entry)

XX DE Mouse J591 monoclonal antibody heavy chain.

XX KW Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
 KW cancer; vascular endothelial cell; metastatic adenocarcinoma.

XX OS Mus sp.

XX PN W09803873-A1.

XX PD 29-JAN-1998.

XX PF 17-JUL-1997; 97WO-US12035.

XX PR 09-APR-1997; 97US-0838682.

XX PR 18-JUL-1996; 96US-0022125.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Bander NH;

XX DR WPI; 1998-120937/11.

XX DR N-PSDB; AAV13949.

XX PT Destroying cancer cells with agent that binds to prostate specific
 PT membrane antigen - on vascular endothelial cells near the cancer, or
 PT on normal, hypertrophic or cancerous prostatic cells, also used for
 PT diagnosis

XX Example 12; Page 53-54; 94pp; English.

XX The present sequence represents the mouse J591 monoclonal antibody heavy
 CC chain from an example of the present invention. The present invention

CC describes the elimination of cancer cells by treating vascular
 CC endothelial cells (VEC) close to the cancer with an agent (A) able to
 CC bind to the extracellular domain (ECD) of prostate specific membrane
 CC antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells.
 CC Also described are: (1) the detection of cancer tissue by detecting
 CC binding of labelled (A) to VEC close to, or within, a cancer tissue; (2)
 CC eliminating or detecting normal, benignly hyperplastic or cancerous
 CC prostate epithelial cells using optionally labelled (A); (3) hybridomas
 CC that produce a monoclonal antibody (MAB) that binds to PSMA. The method
 CC is used to treat renal, urothelial, colon, lung, rectal or breast
 CC cancers and metastatic adenocarcinoma of the liver. The diagnostic
 CC method is particularly used to detect recurrence of prostatic disease or
 CC to monitor the effect of treatments for prostate cancer (presence of
 CC PSMA in the serum indicates that prostate cells are being lysed). (A)
 CC binds to an epitope of PSMA expressed on live cells (contrast antibody
 CC 7E11 which only binds after cell lysis), allowing targeting of live,
 CC unfixed cells and thus providing more efficient treatment and diagnosis.
 CC Both cancer cells themselves and the VEC on which they depend are
 CC killed. All VEC close to cancer cells express PSMA, whatever the type of
 CC cancer, but normal VEC do not.

XX Sequence 130 AA;

Query Match 100.0%; Score 619; DB 19; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.5e-47;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLQSGPELVKPGTSTSRISCKTSGYTFEYTIHWYKQSHGKSLWIGNINPNNGGTTY 60
 Db 11 EVQLQSGPELVKPGTSTSRISCKTSGYTFEYTIHWYKQSHGKSLWIGNINPNNGGTTY 70
 Qy 61 NQFEDKATLTVDKSSSTAYMELSLTSEDSAVYCAAGNFDYWGOGTTLTVSS 115
 Db 71 NQFEDKATLTVDKSSSTAYMELSLTSEDSAVYCAAGNFDYWGOGTTLTVSS 125

RESULT 5

AAV90368

ID AAV90368 standard; Protein; 130 AA.

XX AC AAV90368;

XX DT 15-JAN-2001 (first entry)

XX DE J591 monoclonal antibody heavy chain protein sequence #2.

XX KW J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
 KW prostate specific membrane antigen; prostate cancer; heavy chain.

XX OS Homo sapiens.

XX PN US6107090-A.

XX PD 22-AUG-2000.

XX PF 09-APR-1997; 97US-0838682.

XX PR 06-MAY-1996; 96US-0016976.

XX PR 18-JUL-1996; 96US-0022125.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Bander NH;

XX DR WPI; 2000-571325/53.

XX DR N-PSDB; AAA37831.

XX PT Antibody specific for extracellular prostate-specific membrane antigen,
 PT useful for diagnosis and treatment of prostate cancer

XX Example 12; Fig 7; 33pp; English.

XX This sequence is the heavy chain of the monoclonal antibody J591.

CC The invention relates to an isolated antibody or its antigen binding
 CC portion (I) which binds to an extracellular domain of prostate specific
 CC membrane antigen and which does not require cell lysis to bind to the
 CC extracellular domain. The antibody or its antigen binding portion is
 CC selected for its ability to bind to live cells. (I) is useful for
 CC diagnosis of diseases associated with the presence of normal, benign
 CC hyperplastic, and cancerous epithelial cells or portions. Also it can be
 CC used for identifying the recurrence of such diseases, particularly when
 CC the disease is localised in a particular biological material of the
 CC patient for e.g. recurrence of prostatic disease. They can also be used
 CC alone or bound to a substance effective to kill cancerous prostate
 CC epithelial cells as a therapy for prostate cancer. Binding and
 CC internalising of the antibody with the prostate specific membrane
 CC antigen, permits the therapeutic use of intracellularly acting cytotoxic
 CC agents. (I) targets only prostate epithelial cells and other tissue are
 CC spared which provides safer treatment particularly for elderly patients.
 CC The antibodies bind to living prostate cells and treatments using these
 CC antibodies are more effective than those which target lysed prostate
 CC cells.

XX Sequence 130 AA;
 Query Match 100.0%; Score 619; DB 21; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.5e-47;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFTEYTIHWKQSHGKSLWIGNINPNNGGTTY 60
 DB 11 EVLOQSGPELVKPGTSVRISCKTSGYTFTEYTIHWKQSHGKSLWIGNINPNNGGTTY 70
 QY 61 NOKFEDKATLTVDKSSSTAYMELRLTSDSAVYYCAAGWDFYWGQGTTLTVSS 115
 DB 71 NOKFEDKATLTVDKSSSTAYMELRLTSDSAVYYCAAGWDFYWGQGTTLTVSS 125

RESULT 6
 AAB36219
 ID AAB36219 standard; Protein; 130 AA.
 XX
 AC AAB36219;
 DT 15-FEB-2001 (first entry)
 XX
 DE Murine heavy chain monoclonal antibody J591 #2.
 KW Mouse; antibody; heavy chain; prostate cancer; biological agent.
 XX
 OS Mus sp.

XX US6136311-A.
 XX 24-OCT-2000.
 XX
 XX 17-JUL-1997; 97US-0895914.
 XX
 PR 06-MAY-1996; 96US-0016976.
 PR 18-JUL-1996; 96US-0022125.
 PR 09-APR-1997; 97US-0838682.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Bander NH;
 XX
 DR WPI; 2001-040234/05.
 DR N-PSDB; AAC66538.
 XX
 XX Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating
 PT or killing cancerous, especially non-prostate, cells (e.g. breast
 PT cancerous cells or cancerous cells of metastatic adenocarcinoma to the
 PT liver) .
 XX
 PS Example 12; Fig 7; 35pp; English.
 XX

CC The present invention describes a method of killing cancer cells,
 CC particularly prostate cancer cells, by directing a biological agent to
 CC the cells which then binds to a prostate specific membrane antigen and
 CC causes the molecule to be internalised. The internalisation of the agent,
 CC which may be bound to a drug or which may act to kill the cell alone,
 CC then leads to the death of the cell. The present sequence forms
 CC part of an antibody which may be used as the biological agent of the
 CC invention. In addition to prostate cancer, the method can be used with
 CC renal, urothelial, colon, renal, lung and breast cancer cells, and
 CC cancerous cells of metastatic adenocarcinoma to the liver.

XX Sequence 130 AA;
 Query Match 100.0%; Score 619; DB 22; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.5e-47;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFTEYTIHWKQSHGKSLWIGNINPNNGGTTY 60
 DB 11 EVLOQSGPELVKPGTSVRISCKTSGYTFTEYTIHWKQSHGKSLWIGNINPNNGGTTY 70
 QY 61 NOKFEDKATLTVDKSSSTAYMELRLTSDSAVYYCAAGWDFYWGQGTTLTVSS 115
 DB 71 NOKFEDKATLTVDKSSSTAYMELRLTSDSAVYYCAAGWDFYWGQGTTLTVSS 125

RESULT 7
 AAW37085
 ID AAW37085 standard; Protein; 301 AA.
 XX
 AC AAW37085;
 DT 14-JUL-1998 (first entry)
 XX
 DE Anti-human SC single chain Fv/protamine fusion protein.
 XX
 KW Fusion protein; SC single chain Fv/protamine fusion protein; SECR;
 KW exogenous gene; serpin enzyme complex receptor; gene therapy;
 KW target binding moiety.

XX Homo sapiens.
 OS Mus sp.
 XX
 XX WO9746100-A1.
 XX
 XX 11-DEC-1997.
 XX
 XX 03-JUN-1997; 97WO-US09858.
 XX
 XX 03-JUN-1996; 96US-0656906.
 XX
 XX (UYCA-) UNIV CASE WESTERN RESERVE.
 XX
 XX Davis PB, Ferkol TW, Zlady A;
 XX
 DR WPI; 1998-041783/04.
 DR N-PSDB; AAV00611.
 XX
 PT Delivering compacted exogenous nucleic acid to cells - by targeting
 PT the serpin enzyme complex receptor, used in gene therapy
 XX
 XX Example 9; Pages 120-121; 158pp; English.

XX This represents an anti-human SC single chain Fv/protamine fusion protein
 CC sequence containing a target binding moiety capable of binding to a
 CC serpin enzyme complex receptor (SECR), and a nucleic acid binding moiety.
 CC This can be used in a method for delivering an oligonucleotide to a
 CC mammalian cell. The method comprises conjugating the target binding
 CC moiety to a nucleic acid binding moiety to form a carrier and coupling
 CC the carrier to an expression vector encoding one or more gene products
 CC to form a pharmaceutical composition. A mammalian cell having on its
 CC surface SECR, is contacted with the pharmaceutical composition under
 CC conditions allowing binding to the receptor resulting in delivery of the

pharmaceutical composition to the interior of the cell. The composition and method are used for the introduction of exogenous genetic material into target host cells expressing SCER on their surface. The nucleic acid may encode a functional wild-type or mutant gene or may be an antisense sequence or other nucleic acid having a therapeutic effect. The fusion protein may comprise a protein portion having therapeutic properties, e.g. enzymatic activity, cytokine activity and antibiotic activity, which is delivered to a cell surface via the SCER binding moiety. The nucleic acid can be compacted at high concentrations with the carrier molecule at a critical salt concentration. The condensation of such complexes provides structural features to the DNA/cationic lipid complex that prolong in vivo expression.

QA	Sequence	301 AA;
SQ	Query Match	83.5%; Score 517; DB 19; Length 301;
	Best Local Similarity	81.0%; Pred. No. 6.3e-38;
	Matches	98; Conservative 8; Mismatches 9; Indels 6; Gaps 1;
QY	1	EVLQQSGPLVPCTSVRISCKTSGYTTFEYTIHHWKQSHGKSLSEIWNPNNGTTY 60 : : : : : : : : : : :
Db	127	EVLQQSGPLVPRPGASVKISCKTSGYTFEYTMHWKYQSHGKSLSEIWNPNNGTST 186 : : : : : : : : : :
QY	61	NQKFEDKATLTVDKSSSTAYMELRLTSEDSAVYYCAAGNWF-----DYWGCGTTLTVS 114 : : : : : : : : : :
Db	187	NQKFEGKATLTVDKSSTAYMELRLTSEDSAVYSARYRYDVLSDMWGGCITLTVS 246 : : : : : : : : : :
QY	115	S 115
Db	247	S 247

RESULT 8	
AARI2356	
ID	AARI2356 standard; Protein; 141 AA.
XX	
AC	AARI2356;
XX	
DT	15-AUG-1991 (first entry)
XX	
DE	Heavy chain variable region of murine 2G12 immunoglobulin.
XX	
KW	Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX	
OS	Mus musculus.
XX	
PN	WO9107493-A.
XX	
PD	30-MAY-1991.
XX	
PF	13-NOV-1990; 90WO-US066615.
XX	
PR	13-NOV-1989; 89US-0433730.
XX	
PA	{XOMA-} XOMA CORP.
PA	{GREC } GREEN CROSS CORP.
XX	
PI	Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
XX	
DR	WPI; 1991-178044/24.
DR	N-PSDB; AAQ12058.
XX	
PT	New chimeric mouse-human antibodies - used to detect, kill and
PT	remove HIV-1 antigen from sample
XX	
PS	Disclosure; fig 7; 107pp; English.
XX	
CC	This is the heavy-chain variable (V) region of a mouse monoclonal
CC	antibody (MAB), 2G12, and is specific for an HIV-1 viral antigen.
CC	It is used in the construction of a chimeric MAB comprising heavy
CC	and light chains having murine V regions and human C regions.
CC	The chimeric MABs are more effective than murine MAB 2G12 since
CC	they have an increased compatibility in humans. The heavy and

light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAb's can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV.

Query Match	83.4%	Score 516.5	DB 12	Length 141
Best Local Similarity	80.3%	Pred. No. 3.le-38		
Matches	98	Conservative 8	Mismatches 9	Indels 7
				Gaps 1
QY	1	EVOLQSGPELVKPGCTSVRI	SKTSGYTFEYTIHWVKQSHG	KSLEWGINPNNGGTTY 60
Db	20	EVOLQSGPELVKPGASVKIS	CKTSGYTFEYTIHWVKQSHG	OSLEWGINPNNGGTTY 79
QY	61	NQKPFDKATLTVDKSSSTAY	MELRSLTSDS	SAVYCAAGWN-----FDYWGQGTTLTV 113
Db	80	NQKPFDKATLTVDKSSSTAY	MDVSLTSDS	SAVYCYARRGNLYYGNFWAYWGQGLPTV 139
QY	114	SS 115		
		1:		
Db	140	SA 141		

RESULT 9
AAR12234
ID AAR12234 standard; Protein; 140 AA.

```

Query Match      83.3%; Score 515.5; DB 12; Length 140;
Best Local Similarity 81.0%; Pred. No. 3.7e-38;
Matches 98; Conservative 7; Mismatches 9; Indels 7; Gaps 1;

Qy 1 EVQLQSGPELVKPGTSLVIRCKTSQGTFTFTYTHHWYQSISGLSWIGNINPNNGTTY 60
      |||||

```

```

Db      20 EVLOQSGPDLVKPGASVKISCKTGYTFTETVTHHWKSHGSLWIGGINPNNGGTTY 79
QY      61 NQKFDKATLTVDKSSSTAYMELRSLTSDSAVYYCAAGWN-----FDYWGQGTTLV 113
      80 NQKFDKATLTVDKSSSTAYMDVRSLSLSDSAVYYCARRGNLYYGNFWFAYWGQGPLVIV 139
QY      114 S 114
      140 S 140

RESULT 10
AAR55122
ID      AAR55122 standard; Protein; 118 AA.
XX
AC
XX
DT      27-JAN-1995 (first entry)
XX
DE      Mouse anti-HIV mu5.5 heavy chain variable region.
XX
KW      Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW      human immunodeficiency virus; variable region; VH chain; murine.
XX
OS      Mus musculus.
XX
FH      Key
FT      Region
FT      Location/Qualifiers
FT      1..30
FT      /label= FR1
FT      Region
FT      31..35
FT      /label= CDR1
FT      Region
FT      36..49
FT      /label= FR2
FT      Region
FT      50..66
FT      /label= CDR2
FT      Region
FT      67..98
FT      /label= FR3
FT      Region
FT      99..107
FT      /label= CDR3
FT      Region
FT      108..118
FT      /label= FR4
XX
PN      JP06125783-A.
XX
PD      10-MAY-1994.
XX
PF      28-DEC-1991; 91JP-0359808.
XX
PR      28-DEC-1991; 91JP-0359808.
XX
PA      (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
XX
DR      WPI; 1994-187942/23.
DR      N-PSDB; AAQ65553.
XX
PT      Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT      and recombinant antibody consisting of the H- and L-chains,
PT      useful in AIDS therapy
XX
PS      Example 3; Fig 3; 22pp; Japanese.
XX
CC      Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC      The heavy and light chain variable regions from these antibodies
CC      were sequenced (AAR55120-R55123). The murine anti-HIV CDRs were
CC      introduced into human framework regions to construct chimeric
CC      antibodies (AAR55124-R55127).
XX
SQ      Sequence 118 AA;
      Query Match 82.0%; Score 507.5; DB 15; Length 118;
      Best Local Similarity 81.4%; Pred. No. 1.6e-37;
      Matches 96; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

```

```

QY      1 EVLOQSGPDLVKPGTSVRISCKTSYTFETVTHHWKSHGSKSLWIGNINPNNGGTTY 60
      1 EVLOQSGPDLVKPGASVKISCKTGYTFTETVTHHWKSHGSLWIGGINPNNGGTYSY 60
QY      61 NQKFDKATLTVDKSSSTAYMELRSLTSDSAVYYCAA---GNFDYWGQGTTLTVSS 115
      61 TQKFKGKATLTVDKSSSTAYMELRSLTSDSAVYYCATPYAYAYIDSWGQGTSVTVSS 118

RESULT 11
AAR60301
ID      AAR60301 standard; Protein; 118 AA.
XX
AC      AAR60301;
XX
DT      09-MAR-1995 (first entry)
XX
DE      Anti HIV antibody heavy chain variable region.
XX
KW      Antibody; heavy chain; light chain; human immunodeficiency virus;
KW      HIV; acquired immune deficiency syndrome; AIDS; treatment;
KW      prophylaxis; Mus musculus; Homo sapiens.
XX
OS      Mus musculus.
XX
FH      Key
FT      Region
FT      Location/Qualifiers
FT      1..30
FT      /label= Framework region 1.
FT      Region
FT      31..35
FT      /label= CDR1.
FT      Region
FT      36..49
FT      /label= Framework region 2.
FT      Region
FT      50..66
FT      /label= CDR2.
FT      Region
FT      67..98
FT      /label= Framework region 3.
FT      Region
FT      99..107
FT      /label= CDR3.
FT      Region
FT      108..118
FT      /label= Framework region 4.
XX
PN      WO9415969-A.
XX
PD      21-JUL-1994.
XX
PF      14-JAN-1993; 93WO-JP000039.
XX
PR      14-JAN-1993; 93AU-0032671.
PR      14-JAN-1993; 93WO-JP000039.
XX
PA      (KAGA ) CHEMAO SERO THERAPEUTIC RES INST.
XX
DR      Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
DR      Tokiyoshi S;
XX
DR      WPI; 1994-249145/30.
DR      N-PSDB; AAQ70371.
XX
PT      Recombinant chimeric anti HIV antibody - useful for the treatment
PT      and prevention of HIV
XX
PS      Claim 12; Figure 3; 51pp; Japanese.
XX
CC      The recombinant antibody light chain has neutralising activity
CC      against HIV. Chimeric antibodies comprising both mouse and human
CC      sequences are useful in the treatment/prevention of AIDS caused by
CC      HIV.
XX
SQ      Sequence 118 AA;
      Query Match 82.0%; Score 507.5; DB 15; Length 118;
      Best Local Similarity 81.4%; Pred. No. 1.6e-37;
      Matches 96; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

```


XX
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

Region	/label
50	66

FT /label= CDR2
FT 99..145
FT /label= CDR3
PN EP866131-A2.
XX
XX
XX
PD 23-SEP-1998.
XX
XX 20-MAR-1998; 98EP-0302113.
PF
XX
XX 21-MAR-1997; 97JP-0067938.
PR
XX
XX (SANYO) SANKYO CO LTD.
PA
XX
XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;
PI Yonehara S;
PI
XX
XX WPI; 1998-482965/42.
DR
XX
XX

Production of anti-Fas protein humanised antibodies - for use in inducing apoptosis on Fas expressing cells in the treatment of autoimmune diseases, especially rheumatoid arthritis

Example 4; Page 113; 187pp; English.

This is the amino acid sequence of the heavy chain variable region (mature protein) of mouse anti-human Fas antigen monoclonal antibody CH11. The sequence has been compared with an antibody sequence database, and the framework regions were found to show homology to the H chain of human antibody subgroup I. On the basis of this, primers HVH15-1 (see AAV61365) and HCU3.1 (see AAV61366) were designed for use in the amplification of human heavy chain sequences (see AAV6631). The invention relates to novel humanised antibodies comprising humanised light and heavy chains (see AAV1876-81) of CH11. These humanised anti-human Fas antibodies are capable of inducing apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in the treatment of autoimmune disease and chronic rheumatoid arthritis.

SQ Sequence 116 AA;

Query Match 80.4%; Score 497.5; DB 19; Length 116;
Best Local Similarity 81.9%; Pred. No. 1.2e-36;
Matches 95; Conservative 7; Mismatches 13; Indels 1; Gaps 1;
QY 1 EVQLQQSGPELVKPGTSTYRIKCTSGYTFEYTIHWYKQSHGKSLEWIGNINPNNGGTY 60
Db 1 EVQLQQSGPELVKPGASVKISCKASGYTFDYNMHWKQSHGKSLEWIGIYIPYNGGTGY 60
QY 61 NQKFDKATLTVDKSSSTAYMELSLTSEDSAVYYCAAG-WNFDYWGOGTTLTVSS 115
Db 61 NQKFSKATLTVDNSSSTAYMELSLTSEDSAVYCARSYAMDYWGOGTSVTYSS 116

Search completed: July 21, 2003, 13:31:20
Job time : 53.8018 secs

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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:11:26 ; Search time 48.1982 Seconds
(without alignments)
295.816 Million cell updates/sec

Title: US-09-929-546-19

Perfect score: 569

Sequence: 1 DIYMTQSHFMSTSGVDRVS.....COQNSYPLTFGAGTMIDLK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues 908470

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	569	100.0	107	AAW47087	Mouse J591 monoclo
2	569	100.0	107	AAAY90375	J591 monoclonal an
3	569	100.0	107	AAAB36226	Monoclonal antibod
4	528	92.8	108	20 AAY21817	Anti-STX1 light ch
5	526	92.4	115	22A5 IGM light cha	
6	524	92.1	223	5 AAP40031	Kappa anti-carcino
7	524	92.1	247	9 AAP400155	FRs and CDRs from
8	524	92.1	247	9 AAP80156	Biosynthetic antib
9	521	91.6	107	21 AAY79425	Tie2 receptor antia
10	513	90.2	107	22 AAB69665	Murine Fd138-80 an

11	507.5	89.2	213	23	AAU72819	DNA encoding TRA-8
12	507.5	89.2	234	23	AAU72802	TRA-8 light chain.
13	504	88.6	107	15	AAAR55121	Mouse anti-HIV mu3
14	504	88.6	107	15	AAAB60300	Anti HIV antibody
15	482	84.7	112	21	AAAB19746	Erythropoietin rec
16	481.5	84.6	106	22	AAAB60700	H. pylori catalase
17	481.5	84.6	106	22	AAAB6108	H. pylori catalase
18	476	83.7	133	18	AAW21936	Variable light sub
19	476	83.7	133	20	AAV05266	Antibody 24-31 hum
20	471	82.8	107	18	AAW01591	Lead binding Mab 2
21	471	82.8	108	10	AAAP91381	Antibody light cha
22	471	82.8	108	11	AAAR04936	Sequence of human
23	471	82.8	127	16	AAAR76663	Murine ONS-21 anti
24	471	82.8	127	17	AAW04378	Chimeric human/mu
25	471	82.8	450	21	AAV44991	M79scFv-interleuki
26	471	82.8	456	21	AAV44992	M79scFv-interleuki
27	468	82.2	147	18	AAW19576	Mouse anti-idiotyp
28	467	82.1	123	16	AAAR66317	Anti-IL-8 Mab 5.12
29	467	82.1	123	18	AAW42317	Anti IL-8 antibody
30	467	82.1	123	18	AAW31574	Anti IL-8 monoclon
31	467	82.1	123	18	AAW23784	Monoclonal antibod
32	467	82.1	123	19	AAW69305	Murine anti-IL-8 M
33	467	82.1	123	19	AAW40120	Murine monoclonal
34	467	82.1	123	19	AAW33739	Anti IL-8 monoclon
35	467	82.1	123	20	AAV29437	Murine 5.12.14 ant
36	467	82.1	123	21	AAAB30299	Murine anti-IL-8 a
37	467	82.1	123	21	AAV77742	Murine anti-IL-8 a
38	466	81.9	107	20	AAW86140	Protein sequence o
39	466	81.9	108	19	AAW48863	Murine monoclonal
40	466	81.9	132	15	AAAR56961	Mab A33 light cha
41	465.5	81.8	110	17	AAAR52999	Monoclonal antibod
42	465	81.7	237	20	AAW95440	A33/212 single-cha
43	465	81.7	237	21	AAV54836	Linked fusion prot
44	465	81.7	241	20	AAW95441	A33/218 single-cha
45	465	81.7	241	21	AAV54837	Linked fusion prot

ALIGNMENTS

RESULT-1
AAW47087
ID AAW47087 standard; Protein: 107 AA.
XX
AC AAW47087;
XX
DT 26-JUN-1998 (first entry)
XX
DE Mouse J591 monoclonal antibody light chain variable region VK17.
DE
KW Mouse: monoclonal antibody: J591; prostate specific membrane antigen;
KW cancer; vascular endothelial cell; metastatic adenocarcinoma.
XX
OS Mus sp.
PN WO9803873-AA1.
PD 29-JAN-1998.
XX
PF 17-JUL-1997; 97WO-US12035.
PR 09-APR-1997; 97US-0838682.
PR 18-JUL-1996; 96US-0022125.
XX
(CORR) CORNELL RES FOUND INC.
XX
Bander NH;
DR WPI; 1998-120937/11.
DR N-PSDB; AAV13953.
XX
PT Destroying cancer cells with agent that binds to prostate specific
membrane antigen - on vascular endothelial cells near the cancer, or

PT on normal, hypertrophic or cancerous prostatic cells, also used for
PT diagnosis
XX
PS Example 12; Page 61; 94pp; English.
XX
CC The present sequence represents the mouse J591 monoclonal antibody light
CC chain variable region from clone VK17 from an example of the present
CC invention. The present invention describes the elimination of cancer
CC cells by treating vascular endothelial cells (VEC) close to the cancer
CC with an agent (A) able to bind to the extracellular domain (ECD) of
CC prostate specific membrane antigen (PSMA). (A) both binds to the VEC and
CC destroys the cancer cells. Also described are: (1) the detection of
CC cancer tissue by detecting binding of labelled (A) to VEC close to, or
CC within, a cancer tissue; (2) eliminating or detecting normal, benignly
CC hyperplastic or cancerous prostate epithelial cells using optionally
CC labelled (A); (3) hybridomas that produce a monoclonal antibody (MAb)
CC that binds to PSMA. The method is used to treat renal, urothelial,
CC colon, lung, rectal or breast cancers and metastatic adenocarcinoma of
CC the liver. The diagnostic method is particularly used to detect
CC recurrence of prostatic disease or to monitor the effect of treatments
CC for prostate cancer (presence of PSMA in the serum indicates that
CC prostate cells are being lysed). (A) binds to an epitope of PSMA
CC expressed on live cells (contrast antibody 7E11 which only binds after
CC cell lysis), allowing targeting of live, unfixed cells and thus
CC providing more efficient treatment and diagnosis. Both cancer cells
CC themselves and the VEC on which they depend are killed. All VEC close to
CC cancer cells express PSMA, whatever the type of cancer, but normal VEC
CC do not.
XX
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 569; DB 19; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.3e-41;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVMTQSHKFMSTVGDVRSIIICKASQDVGTAVDWYQKPGSPKLLIYWASTRHTGVDP 60
DB 1 DIVMTQSHKFMSTVGDVRSIIICKASQDVGTAVDWYQKPGSPKLLIYWASTRHTGVDP 60
QY 61 RTGSGSGDFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107
DB 61 RTGSGSGDFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107

RESULT 2
AAY90375
ID AAY90375 standard; Protein; 107 AA.
XX
XX AAY90375;
AC
DT 15-JAN-2001 (first entry)
XX
XX J591 monoclonal antibody light chain protein sequence fragment.
XX
XX J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
KW prostate specific membrane antigen; prostate cancer; light chain.
XX
XX Homo sapiens.
XX
XX US6107090-A.
XX
XX 22-AUG-2000.
XX
XX 09-APR-1997; 97US-0838682.
XX
XX 06-MAY-1996; 96US-0016976.
PR 18-JUL-1996; 96US-0022125.
XX
XX (CORR) CORNELL RES FOUND INC.
XX
XX Bander NH;
XX
XX WPI; 2000-571325/53.
DR

DR N-PSDB; AAA37835.
XX
XX Antibody specific for extracellular prostate-specific membrane antigen,
PT useful for diagnosis and treatment of prostate cancer
XX
PS Example 12; Column 24; 33pp; English.
XX
CC This sequence is a fragment of the light chain of the monoclonal antibody
CC J591. The invention relates to an isolated antibody or its antigen
CC binding portion (I) which binds to an extracellular domain of prostate
CC specific membrane antigen and which does not require cell lysis to bind
CC to the extracellular domain. The antibody or its antigen binding portion
CC is selected for its ability to bind to live cells. (I) is useful for
CC diagnosis of diseases associated with the presence of normal, benign
CC hyperplastic, and cancerous epithelial cells or portions. Also it can be
CC used for identifying the recurrence of such diseases, particularly when
CC the disease is localised in a particular biological material of the
CC patient for e.g. recurrence of prostatic disease. They can also be used
CC alone or bound to a substance effective to kill cancerous prostate
CC epithelial cells as a therapy for prostate cancer. Binding and
CC internalising of the antibody with the prostate specific membrane
CC antigen, permits the therapeutic use of intracellularly acting cytotoxic
CC agents. (I) targets only prostate epithelial cells and other tissue are
CC spared which provides safer treatment particularly for elderly patients.
CC The antibodies bind to living prostate cells and treatments using these
CC antibodies are more effective than those which target lysed prostate
CC cells.
XX
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 569; DB 21; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.3e-41;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVMTQSHKFMSTVGDVRSIIICKASQDVGTAVDWYQKPGSPKLLIYWASTRHTGVDP 60
DB 1 DIVMTQSHKFMSTVGDVRSIIICKASQDVGTAVDWYQKPGSPKLLIYWASTRHTGVDP 60
QY 61 RTGSGSGDFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107
DB 61 RTGSGSGDFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107

RESULT 3
AAB36226
ID AAB36226 standard; Protein; 107 AA.
XX
XX AAB36226;
AC
DT 15-FEB-2001 (first entry)
XX
XX Monoclonal antibody J591 kappa light chain V region #2.
DE
DE Mouse; antibody; heavy chain; prostate cancer; biological agent.
KW
XX Mus sp.
OS
XX US6136311-A.
PN
XX 24-OCT-2000.
PD
XX 17-JUL-1997; 97US-0895914.
PF
XX 06-MAY-1996; 96US-0016976.
PR 18-JUL-1996; 96US-0022125.
PR 09-APR-1997; 97US-0838682.
XX
XX (CORR) CORNELL RES FOUND INC.
XX
XX Bander NH;
XX
XX WPI; 2001-040234/05.
DR N-PSDB; AAC66546.

XX Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating
PT or killing cancerous, especially non-prostate, cells (e.g. breast
PT cancerous cells or cancerous cells of metastatic adenocarcinoma to the
PT liver) -
XX
PS Example 12; Column 26; 35pp; English.
XX
PS The present invention describes a method of killing cancer cells.
CC particularly prostate cancer cells, by directing a biological agent to
CC the cells which then binds to a prostate specific membrane antigen and
CC causes the molecule to be internalised. The internalisation of the agent,
CC then leads to the death of the cell. The present sequence forms
CC part of an antibody which may be used as the biological agent of the
CC invention. In addition to prostate cancer, the method can be used with
CC renal, urothelial, colon, renal, lung and breast cancer cells, and
CC cancerous cells of metastatic adenocarcinoma to the liver.
XX
SQ Sequence 107 AA;
Query Match 100.0%; Score 569; DB 22; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.3e-41;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVVTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||
Db 1 DIVVTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||
QY 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMDLX 107
|||||
Db 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMDLX 107
|||||
RESULT 4
AAV21817
ID AAV21817 standard; Protein; 108 AA.
XX
AC AAV21817;
XX
DT 10-SEP-1999 (first entry)
XX
DE Anti-STX1 light chain variable region.
XX
KW Humanised; monoclonal antibody; MAb; Shiga toxin; immunoglobulin;
KW Ig constant region; enterohemorrhagic Escherichia coli; EHEC; uremia;
KW edema; bloody diarrhoea; hemorrhagic colitis; hemolytic uremic syndrome;
KW thrombocytopenia; EHEC-mediated disease; anti-STX1.
XX
OS Shigella dysenteriae.
XX
FH Key Location/Qualifiers
FT Region 24...34
FT /note= "complementarity determining region (CDR) 1;
FT specifically claimed for in claim 10"
FT Region 50..56
FT /note= "complementarity determining region (CDR) 2;
FT specifically claimed for in claim 10"
FT Region 89..97
FT /note= "complementarity determining region (CDR) 3;
FT specifically claimed for in claim 10"
XX
PN WO932645-A1.
XX
PD 01-JUL-1999.
XX
XX 22-DEC-1998; 98WO-US27267.
XX
XX 18-DEC-1998; 98US-0215163.
XX
XX 23-DEC-1997; 97US-0068635.
XX
XX (MELT/) MELTON-CELSA A.
XX (OBRI/) O'BRIEN A D.
XX

PA (SCHM/) SCHMITT C K.
PA (STIN/) STINSON J L.
PA (WONG/) WONG H.
XX
PI Melton-Celsa A, O'Brien AD, Schmitt CK, Stinson JL;
PI Wong H;
XX
DR WPI; 1999-418935/35.
DR N-PSDB; AAX82029.
XX
XX Humanized monoclonal antibodies against Shiga toxins, useful for
PT protection against enterohemorrhagic Escherichia coli or other Shiga
PT toxin producing bacteria
XX
PS Claim 5; Fig 3; 75pp; English.
XX
CC The invention relates to humanised monoclonal antibodies (MAB) against
CC Shiga toxins. The humanised MAB that binds to Shiga toxin comprises a
CC constant and a variable region, where: (a) the constant region contains
CC at least part of a human immunoglobulin (Ig) constant region; and (b) the
CC variable region contains at least part of a non-human Ig variable region.
CC Host cells transformed with vectors encoding a humanised MAB against
CC Shiga toxin type 2 is useful for treating a patient with an infection
CC caused by enterohemorrhagic Escherichia coli (EHEC) or other Shiga toxin
CC producing bacteria. The humanised MAB can also be used to reduce illness
CC caused by EHEC or other Shiga toxin producing bacteria. EHEC are
CC associated with food-borne outbreaks of bloody diarrhoea (hemorrhagic
CC colitis) and the hemolytic uremic syndrome. In particular, the humanised
CC MABs ameliorate edema, thrombocytopenia and uremia associated with EHEC-
CC mediated disease. The present sequence represents an anti-STX1 light
CC chain variable region.
XX
SQ Sequence 108 AA;
Query Match 92.8%; Score 528; DB 20; Length 108;
Best Local Similarity 92.5%; Pred. No. 9.9e-38;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIVVTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||
Db 1 DIVVTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||
QY 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMDLX 107
|||||
Db 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMDLX 107
|||||
RESULT 5
ABB07359
ID ABB07359 standard; Protein; 115 AA.
XX
AC ABB07359;
XX
DT 09-APR-2002 (first entry)
XX
DE 22A5 IgM light chain variable region.
XX
KW Immunoglobulin; Ig; reperfusion; ischaemic injury; pathogenic;
KW vasotropic; antibody; 22A5; IgM.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Misc-difference 109
FT /note= "encoded by TGA"
XX
XX WO200193892-A1.
XX
XX 13-DEC-2001.
XX
XX 08-JUN-2001; 2001WO-US18510.
XX
XX 08-JUN-2000; 2000US-210272P.
XX

XX (BLOO-) CENT BLOOD RES INC.
XX Carroll MC, Moore FD, Hechtman HB;
XX WPI: 2002-139643/18.
XX N-PSDB; ABA94516.
XX Treating or preventing immunoglobulin-mediated reperfusion or ischemic
PT injury resulting from e.g. angioplasty or bypass surgery, by
PT administering an inhibitor of pathogenic immunoglobulin and ischemic
PT antigen interaction
XX
PS Claim 50; Page 73-74; 77pp; English.
XX The invention provides a method of treating or preventing immunoglobulin-
CC mediated reperfusion or ischemic injury in a subject. The method involves
CC administering an inhibitor of an interaction between a pathogenic
CC immunoglobulin, and an ischemic-specific antigen or a component of the
CC complement pathway. The method is useful for treating or preventing
CC immunoglobulin-mediated reperfusion or ischemic injury, in particular,
CC injury that results following a naturally occurring episode, a surgical
CC procedure (e.g. angioplasty, stenting procedure, atherectomy or bypass
CC surgery), or in an injury that occurs in a cardiovascular tissue. The
CC method is also useful for treating or preventing, in a subject, tissue
CC damage following reperfusion caused by a pathogenic immunoglobulin, e.g.
CC pathogenic IgMs. The present sequence represents the light chain variable
CC region of 22A5 IgM, a pathogenic immunoglobulin.
XX
SQ Sequence 115 AA;
Query Match 92.4%; Score 526; DB 23; Length 115;
Best Local Similarity 92.5%; Pred. No. 1.6e-37;
Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 IVMTQSHKFMSTSGVDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRTHTGVPDR 61
DB 1 IVMTQSHKFMSTSGVDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRTHTGVPDR 60
QY 62 FTGSGSGDTFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107
DB 61 FTGSGSGDTFTLTITNVQSEDLADYFCQOYNSYPLTFGSGTKLEIK 106
RESULT 6
AAP40031
ID AAP40031 standard; Protein; 223 AA.
XX AAP40031;
AC AAP40031;
DT 01-DEC-1991 (first entry)
XX Kappa anti-carcinoembryonic antigen chain.
XX Immunoglobulin; carcinoembryonic antigen.
XX
PN EP125023-A.
XX
PD 14-NOV-1984.
XX
PF 06-APR-1984; 84EP-0302368.
XX
PR 08-APR-1983; 83US-0483457.
XX
PA (CITY) CITY OF HOPE.
PA (GETH) GENENTECH INC.
XX
PI Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD;
XX WPI: 1984-283749/46.
DR N-PSDB; AAN40023.
XX
PT Immunoglobulin(s) produced by recombinant host cells - useful as

PT antibodies analogous to forms from mammals.
XX
PS Disclosure; Fig. 3; 79pp; English.
XX
CC The protein is encoded by the mRNA coding sequence of the cDNA fragment
CC contained within recombinant vector pK1764. Using the vector this
CC immunoglobulin is produced readily in pure monoclonal form. Genetic
CC manipulations can be used to produce chimeras of variants drawing their
CC homology from species differing from each other. Protein manipulation
CC is also possible.
XX
SQ Sequence 223 AA;
Query Match 92.1%; Score 524; DB 5; Length 223;
Best Local Similarity 90.7%; Pred. No. 4.4e-37;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIVMTQSHKFMSTSGVDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRTHTGVPD 60
DB 10 DIVMTQSHKFMSTSGVDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRTHTGVPD 69
QY 61 RFTGSGSGDTFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107
DB 70 RFTGSGSGDTFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 116
RESULT 7
AAP80155
ID AAP80155 standard; protein; 247 AA.
XX AAP80155;
AC AAP80155;
DT 13-OCT-1990 (first entry)
XX
DE FRs and CDRs from anti-CEA monoclonal antibody.
XX
KW Biosynthetic Antibody Binding site (BABS); variable domain;
KW anti-CEA monoclonal antibody; ss.
XX
OS Synthetic.
XX
PN WO8809344-A.
XX
PD 01-DEC-1988.
XX
PF 19-MAY-1988; 88WO-US01737.
XX
PR 21-MAY-1987; 87US-0052800.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI Huston JS, Oppermann H;
XX
DR WPI: 1988-353928/49.
DR N-PSDB; AAN80181.
XX
PT Recombinant multifunctional protein - having an Ab binding site and a
PT sequence for biological activity, ion sequestering or binding to a solid
PT support.
XX
PS Disclosure; 15pp; English.
XX
CC Multi-functional biosynthetic protein comprising FRs and
CC CDRs with specificity for a tumour antigen CEA.
CC See also AAN80171-N80192.
XX
SQ Sequence 247 AA;
Query Match 92.1%; Score 524; DB 9; Length 247;
Best Local Similarity 90.7%; Pred. No. 4.8e-37;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIVMTQSHKFMSTSGVDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRTHTGVPD 60


```
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIVMTQSHKFMSTSGVDRVSIICKASQDVGTAVDWYQKPGSPKLLIYWASTRHTGVDP 60
Db 1 DIVMTQSHKFMSTSGVDRVSIICKASQDVGTAVDWYQKPGSPKLLIYWASTRHTGVDP 60
QY 61 RFTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107

RESULT 14
AAR60300
ID AAR60300 standard; Protein; 107 AA.
XX
AC AAR60300;
XX
DT 09-MAR-1995 (first entry)
XX
DE Anti HIV antibody light chain variable region.
XX
KW Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS: treatment;
KW prophylaxis; Mus musculus; Homo sapiens.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 1..23
FT /label= Framework region 1.
FT Region 24..34
FT /label= CDR1.
FT Region 35..49
FT /label= Framework region 2.
FT Region 50..56
FT /label= CDR2.
FT Region 57..88
FT /label= Framework region 3.
FT Region 89..97
FT /label= CDR3.
FT Region 98..107
FT /label= Framework region 4.
XX
PN WO9415969-A.
XX
PD 21-JUL-1994.
XX
PF 14-JAN-1993; 93WO-JP00039.
XX
PR 14-JAN-1993; 93AU-0032671.
PR 14-JAN-1993; 93WO-JP00039.
XX
PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
XX
PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
PI Tokiyoshi S;
XX
DR WPI; 1994-249145/30.
DR N-PSDB; AAQ70370.
XX
PT Recombinant chimeric anti HIV antibody - useful for the treatment
PT and prevention of HIV
XX
PS Claim 7; Figure 2; 51pp; Japanese.
XX
CC The recombinant antibody light chain has neutralising activity
CC against HIV. Chimeric antibodies comprising both mouse and human
CC sequences are useful in the treatment/prevention of AIDS caused by
CC HIV.
XX
SQ Sequence 107 AA;
Query Match 88.6%; Score 504; DB 15; Length 107;
```

```
Best Local Similarity 88.8%; Pred. No. 1..le-35;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIVMTQSHKFMSTSGVDRVSIICKASQDVGTAVDWYQKPGSPKLLIYWASTRHTGVDP 60
Db 1 DIVMTQSHKFMSTSGVDRVSIICKASQDVGTAVDWYQKPGSPKLLIYWASTRHTGVDP 60
QY 61 RFTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLKL 107

RESULT 15
AAB19746
ID AAB19746 standard; Protein; 112 AA.
XX
AC AAB19746;
XX
DT 19-FEB-2001 (first entry)
XX
DE Erythropoietin receptor agonist MAb 3G9 VL region.
XX
KW Erythropoietin receptor; agonist; monoclonal antibody; MAb; mouse;
KW light chain variable region; antibody engineering; erythropoiesis;
KW anaemia; cytopenia; acute renal failure; antianaemic; therapy;
KW complementarity determining region; CDR.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region 24..34
FT /label= CDR1
FT Region 50..56
FT /label= CDR2
FT Region 89..97
FT /label= CDR3
XX
PN WO2000061637-A1.
XX
PD 19-OCT-2000.
XX
PF 14-APR-2000; 2000WO-US10284.
XX
PR 14-APR-1999; 99US-0129263.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Erickson-Miller CL, Holmes SD, Taylor AH, Young PR;
XX
DR WPI; 2000-679469/66.
DR N-PSDB; AAA88853.
XX
PT Novel erythropoietin receptor agonist antibody useful for enhancing
PT erythropoiesis in the treatment of anemia, cytopenia or acute renal
PT failure
XX
PS Claim 6; Page 50; 70pp; English.
XX
CC The present sequence is that of the light chain variable region
CC (VL) of 3G9, a murine monoclonal antibody (MAb) produced by hybridoma
CC cell line 3G9. MAb 3G9 competes with erythropoietin for binding to
CC the erythropoietin receptor (EpoR), and is characterised by agonist
CC activity on erythrocyte production. A claimed EpoR agonist antibody
CC comprises the 3G9 VL and VH (see AAB19745) regions. MAb 3G9 can also
CC be used for the development of EpoR agonist humanised antibodies
CC that incorporate 3G9 VH and VL complementarity determining regions
CC within human frameworks. The EpoR agonist antibodies are used in a
CC claimed method for enhancing erythropoiesis, for the treatment of
CC anaemia, cytopenia, acute renal failure, and other conditions with
CC depressed erythrocyte production. Agonist antibodies of EpoR have
CC the same therapeutic utility as the natural ligand, but with the
CC advantages of easier purification and longer half-life in vivo.
XX
```

Db 1 DIVMTQSHKFMSTSVGDRVSITCKASQDVCTAVAWYQOKPGQSPKLIYWASTRHTGVPD 60
Qy 61 RFTGSGSGTDTLTITNVQSEDADYFCQOYNSYPLTFEGAGTMDLX 107
|||||
Db 61 RFTGSGSGTDTLTITNVQSEDADYFCQOYNSY-RTFGGKTLEIK 106
|||||
RESULT 12
AAU72802
ID AAU72802 standard; Protein; 234 AA.
XX
AC AAU72802:
XX
DT 26-FEB-2002 (first entry)
XX
DE TRA-8 light chain.
XX
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor;
KW TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
OS Mus musculus.
XX
PN WO200183560-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14151.
XX
PR 02-MAY-2000; 2000US-201344P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
DR WPI: 2002-049338/06.
DR N-PSDB; AAS97063.
XX
PT Novel antibody specific for tumour necrosis factor-related
PT apoptosis-inducing ligand, useful for inhibiting cell proliferation in
PT cancer -
XX
PS Claim 30; Page 200; 229pp; English.
XX
CC The invention describes a novel antibody which recognizes a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or
CC dysregulated cells, and for inhibiting cell proliferation in a cell,
CC preferably a human breast, ovary, colon, haematopoietic, prostate,
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC antibody is used to treat an autoimmune disease, systemic lupus
CC erythematosus, Hashimoto's disease, rheumatoid arthritis,
CC graft-versus-host disease, Sjogren's syndrome, Chron's disease,
CC pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple
CC sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,
CC allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerular nephritis, hypoplastic anaemia, rejection after organ
CC transplantation, and numerous malignancies of lung, prostate, liver,
CC ovary, lymphatic or breast tissue. Peptides used to design primers for
CC isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and
CC AAU72802), TRA-8 are shown in AAU72799 and AAU72800.
XX
SQ Sequence 234 AA;

Query Match 89.2%; Score 507.5; DB 23; Length 234;
Best Local Similarity 90.7%; Pred. No. 1.1e-35;
Matches 97; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
Qy 1 DIVMTQSHKFMSTSVGDRVSITCKASQDVCTAVAWYQOKPGQSPKLIYWASTRHTGVPD 60
|||||
Db 22 DIVMTQSHKFMSTSVGDRVSITCKASQDVCTAVAWYQOKPGQSPKLIYWASTRHTGVPD 81
|||||
Qy 61 RFTGSGSGTDTLTITNVQSEDADYFCQOYNSYPLTFEGAGTMDLX 107
|||||
Db 82 RFTGSGSGTDTLTITNVQSEDADYFCQOYNSY-RTFGGKTLEIK 127
|||||
RESULT 13
AAR55121
ID AAR55121 standard; Protein; 107 AA.
XX
AC AAR55121;
XX
DT 27-JAN-1995 (first entry)
XX
DE Mouse anti-HIV mu39.1 light chain variable region.
XX
KW Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW human immunodeficiency virus; variable region; VH chain; murine.
XX
OS Mus musculus.
XX
FH Key
FT Region 1..23
FT /label= FR1
FT Region 24..34
FT /label= CDR1
FT Region 35..49
FT /label= FR2
FT Region 50..56
FT /label= CDR2
FT Region 57..88
FT /label= FR3
FT Region 89..97
FT /label= CDR3
FT Region 98..107
FT /label= FR4
XX
PN JP06125783-A.
XX
PD 10-MAY-1994.
XX
XX 28-DEC-1991; 91JP-0359808.
XX
PR 28-DEC-1991; 91JP-0359808.
XX
XX (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
XX
XX WPI: 1994-187942/23.
XX N-PSDB; AAQ65552.
XX
PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
PT and recombinant antibody consisting of the H- and L-chains,
PT useful in AIDS therapy
XX
XX Example 3; Fig 2; 22pp; Japanese.
XX
CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
CC The heavy and light chain variable regions from these antibodies
CC were sequenced (AAR55120-R55123). The murine anti-HIV CDRs were
CC introduced into human framework regions to construct chimeric
CC antibodies (AAR55124-R55127).
XX
SQ Sequence 107 AA;
Query Match 88.6%; Score 504; DB 15; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.1e-35;

SQ Sequence 112 AA;

Query Match	84.7%	Score 482;	DB 21;	Length 112;
Best Local Similarity	86.0%;	Pred. No. 8.2e-34;		
Matches 92;	Conservative	7;	Mismatches 8;	Indels 0; Gaps 0;

Qy 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60

Dbb 1 DIVMTQSQKFMTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKALIYSASRYSGVPD 60

QY 61 RFTGSGSGTDFLTITNVQSEDLADYFCQVNSYPLTFGAGTMLDLK 107

D**b** 61 RFTGSGSGTDFTLTISNVQSEDLAEYFCQVNSYPLTFGACTKLELK 107

Search completed: July 21, 2003, 13:31:21

Job time : 49.1982 secs

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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:20:30 ; Search time 12.4324 Seconds
(without alignments)
272.162 Million cell updates/sec

Title: us-09-929-546-8

Perfect score: 619

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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	619	100.0	115	3	US-08-838-682-8
2	619	100.0	115	4	US-08-895-914-8
3	619	100.0	115	4	US-09-357-710A-8
4	619	100.0	130	3	US-08-838-682-4
5	619	100.0	130	4	US-08-895-914-4
6	619	100.0	130	4	US-09-357-710A-4
7	517	83.5	301	2	US-08-656-906-25
8	517	83.5	301	4	US-09-217-847-25
9	507.5	82.0	118	1	US-08-491-845-6
10	499.5	80.7	128	1	US-08-202-047-21
11	499.5	80.7	128	3	US-08-964-690-21
12	496	80.1	117	4	US-08-525-539A-76
13	496	80.1	136	4	US-08-525-539A-47
14	494.5	79.9	139	2	US-08-116-778E-1
15	494.5	79.9	139	2	US-08-438-562-1
16	494.5	79.9	139	2	US-08-483-528B-91
17	494.5	79.9	233	3	US-08-444-644-33
18	494.5	79.9	233	3	US-08-232-246A-33
19	494.5	79.9	233	3	US-08-444-644-19
20	494.5	79.9	235	3	US-08-444-644-28
21	494.5	79.9	235	3	US-08-444-644-42
22	494.5	79.9	235	4	US-08-232-246A-19
23	494.5	79.9	235	4	US-08-232-246A-28
24	494.5	79.9	235	4	US-08-232-246A-42
25	493.5	79.7	232	1	US-08-425-763-2
26	493.5	79.7	232	3	US-08-811-757-2
27	493.5	79.7	232	4	US-09-249-230-2

28	492.5	79.6	116	1	US-07-634-278-56	Sequence 56, Appl
29	492.5	79.6	116	1	US-08-477-728-56	Sequence 56, Appl
30	492.5	79.6	116	1	US-08-474-040-56	Sequence 56, Appl
31	492.5	79.6	116	1	US-08-487-200-56	Sequence 56, Appl
32	492.5	79.6	116	4	US-08-484-537-56	Sequence 56, Appl
33	492.5	79.6	135	1	US-07-634-278-69	Sequence 69, Appl
34	492.5	79.6	135	1	US-08-477-728-69	Sequence 69, Appl
35	492.5	79.6	135	1	US-08-474-040-69	Sequence 69, Appl
36	492.5	79.6	135	1	US-08-487-200-69	Sequence 69, Appl
37	492.5	79.6	135	4	US-08-484-537-69	Sequence 69, Appl
38	491.5	79.4	143	4	US-09-301-593-26	Sequence 26, Appl
39	491.5	79.4	472	4	US-09-301-593-30	Sequence 30, Appl
40	491	79.3	125	4	US-09-357-710A-20	Sequence 20, Appl
41	490.5	79.2	454	2	US-07-934-373C-22	Sequence 22, Appl
42	490.5	79.2	454	3	US-08-437-642B-22	Sequence 22, Appl
43	490.5	79.2	454	4	US-08-146-206C-22	Sequence 22, Appl
44	490.5	79.2	454	5	PCT-US93-07832-22	Sequence 22, Appl
45	489.5	79.1	135	1	US-08-137-117D-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-838-682-8
; Sequence 8, Application US/08838682
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-682-8

Query Match 100.0%; Score 619; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.le-53;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKPGTSSVRIKCTSGYTFTEYTHHWKQSHGKSLWIGNINPNNGGTY 60
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Db 1 EVLOQSGPELVKPGTSSVRIKCTSGYTFTEYTHHWKQSHGKSLWIGNINPNNGGTY 60
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QY 61 NQKPEDKATLTVDKSSSTAYMELRLTSDSVAVYCAAGWNFYDYGQGTTLTVSS 115
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Db 61 NQKPEDKATLTVDKSSSTAYMELRLTSDSVAVYCAAGWNFYDYGQGTTLTVSS 115
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RESULT 2

US-08-895-914-8
; Sequence 8, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,914
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,682
; FILING DATE: 09-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-895-914-8

Query Match 100.0%; Score 619; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.le-53;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKPGTSSVRIKCTSGYTFTEYTHHWKQSHGKSLWIGNINPNNGGTY 60
|||||
Db 1 EVLOQSGPELVKPGTSSVRIKCTSGYTFTEYTHHWKQSHGKSLWIGNINPNNGGTY 60
|||||
QY 61 NQKPEDKATLTVDKSSSTAYMELRLTSDSVAVYCAAGWNFYDYGQGTTLTVSS 115
|||||
Db 61 NQKPEDKATLTVDKSSSTAYMELRLTSDSVAVYCAAGWNFYDYGQGTTLTVSS 115
|||||

RESULT 3

US-09-357-710A-8
; Sequence 8, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: B2L 242/025
; CURRENT APPLICATION NUMBER: US/09/357,710A
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-8

Query Match 100.0%; Score 619; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.le-53;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVLOQSGPELVKPGTSSVRIKCTSGYTFTEYTHHWKQSHGKSLWIGNINPNNGGTY 60
|||||
Db 1 EVLOQSGPELVKPGTSSVRIKCTSGYTFTEYTHHWKQSHGKSLWIGNINPNNGGTY 60
|||||
QY 61 NQKPEDKATLTVDKSSSTAYMELRLTSDSVAVYCAAGWNFYDYGQGTTLTVSS 115
|||||
Db 61 NQKPEDKATLTVDKSSSTAYMELRLTSDSVAVYCAAGWNFYDYGQGTTLTVSS 115
|||||

RESULT 4

US-08-838-682-4
; Sequence 4, Application US/08838682
; Patent No. 6107050
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/656,906
FILING DATE: 03-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 03-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/25809
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/216,534
FILING DATE: 23-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CASE-02280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-656-906-25

Query Match 83.5%; Score 517; DB 2; Length 301;
Best Local Similarity 81.0%; Pred. No. 3.3e-43;
Matches 98; Conservative 8; Mismatches 9; Indels 6; Gaps 1;
QY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFEYTHHWKSHGKSLWIGNINPNNGGTTY 60
DB 127 EVLOQSGPDLVKPGASVKISCKTSGYTFEYTHHWKSHGKSLWIGNINPNNGGTSY 186
QY 61 NQKPEDKATLVKSSSTAYMELRLTSDSAVYCAAGWNP-----DYWGQGTTLTVS 114
DB 187 NQKFGKATLVKSSSTAYMELRLTSDSAVYCAAGWNP-----DYWGQGTTLTVS 246
QY 115 S 115
DB 247 S 247

RESULT 8
US-09-217-847-25
Sequence 25, Application US/09217847
Patent No. 6200801
GENERAL INFORMATION:
APPLICANT: Ferkol Jr., Thomas W.
APPLICANT: Davis, Pamela B.
APPLICANT: Zlady, Assem-Galal
TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
TITLE OF INVENTION: Mediated Gene Transfer
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,847
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/656,906

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/25809
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/216,534
FILING DATE: 23-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CASE-02280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-217-847-25

Query Match 83.5%; Score 517; DB 4; Length 301;
Best Local Similarity 81.0%; Pred. No. 3.3e-43;
Matches 98; Conservative 8; Mismatches 9; Indels 6; Gaps 1;
QY 1 EVLOQSGPELVKPGTSVRISCKTSGYTFEYTHHWKSHGKSLWIGNINPNNGGTTY 60
DB 127 EVLOQSGPDLVKPGASVKISCKTSGYTFEYTHHWKSHGKSLWIGNINPNNGGTSY 186
QY 61 NQKPEDKATLVKSSSTAYMELRLTSDSAVYCAAGWNP-----DYWGQGTTLTVS 114
DB 187 NQKFGKATLVKSSSTAYMELRLTSDSAVYCAAGWNP-----DYWGQGTTLTVS 246
QY 115 S 115
DB 247 S 247

RESULT 9
US-08-491-845-6
Sequence 6, Application US/08491845
Patent No. 5773247
GENERAL INFORMATION:
APPLICANT: MAEDA, Hiroaki
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: EDA, Yasuyuki
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,845
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:

```
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MAEDA-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-491-845-6

Query Match      82.0%; Score 507.5; DB 1; Length 118;
Best Local Similarity 81.4%; Pred. No. 9.4e-43;
Matches 96; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

Qy 1 EVLOQSGPELVKPGTSVRISCKTSGYTFEYTIHWVKQSHGKSLEWIGNINPNNGTTY 60
Db 1 EVLOQSGPELVKPGASVKISCKTSGYTFEYTMHWVKQSHGSRLEWIGGINPNNGDTSY 60
Qy 61 NQKFEKATLVKSSSTAYMELRSLTSDSAVYYCAA-----GNFDYWGQTTLTVSS 115
Db 61 TQKFKGKATLVKSSSTAYMELRSLTSDSAVYYCATPYAYAYDAISWGQTSVTYSS 118

RESULT 10
US-08-202-047-21
; Sequence 21, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to p-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/202,047
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label- MOUSE_IIA
; US-08-964-690-21

Query Match      80.7%; Score 499.5; DB 3; Length 128;

; OTHER INFORMATION: /label- MOUSE_IIA
; US-08-202-047-21

Query Match      80.7%; Score 499.5; DB 1; Length 128;
Best Local Similarity 75.0%; Pred. No. 6.3e-42;
Matches 96; Conservative 10; Mismatches 9; Indels 13; Gaps 1;

Qy 1 EVLOQSGPELVKPGTSVRISCKTSGYTFEYTIHWVKQSHGKSLEWIGNINPNNGTTY 60
Db 1 EVLOQSGPELVKPGASVKISCKASGYTFDYTMWVKQSPGKSLEWIGDINPCNGGTSY 60
Qy 61 NQKFEKATLVKSSSTAYMELRSLTSDSAVYYCAAG-----WNFDYWGQ 107
Db 61 NQKFKGKATLVKSSSTAYMOLSLTSDSAVYYCARGYYSSSYMAXXYAFDYWGQ 120
Qy 108 GTTTLTVSS 115
Db 121 GTTTLTVSS 128

RESULT 11
US-08-964-690-21
; Sequence 21, Application US/08964690
; Patent No. 6033667
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to p-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/964,690
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label- MOUSE_IIA
; US-08-964-690-21

Query Match      80.7%; Score 499.5; DB 3; Length 128;
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Best Local Similarity    75.08;   Pred. No. 6.3e-42;  
Matches      96; Conservative     10; Mismatches       9; Indels      13; Gaps        1  
  
QY          1 EVOLQQSGPELVKPGTGVRRISCKTSGYTFEYTHWVKQSHGKSLEWTGNTPNNGGTYY 60  
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Db          1 EVOLQQSGPELVKPGASVKKISKRASGYFTDYNNWKSPGKSLIEWIGDINPQGGSY 60  
              ||||| :|||| |::||| ||||| ||||| |||||  
  
QY         61 NQKFEDRATLTVDKSSSTAYNELRLSLSFSDSAVIYCAG-----WNFDYWGG 107  
              ||||| :||||| ||||| ||||| ||||| |||||  
Db         61 NQKFKGRATLTVDKSSSTAYMQLSSLTSFSDSAVICARGXYSSSYMAXXXYPFYWGQ 120  
              ||||| :||||| ||||| ||||| ||||| |||||  
  
QY        108 GTTLTVSS 115  
               |||:||||  
Db        121 GTTTVTSS 128
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RESULT 12
 US-08-525-539A-76
 : Sequence.76, Application US/08525539A
 : Patent No. 6309636
 : GENERAL INFORMATION:
 : APPLICANT: DO COUTO, FERNANDO J.R.
 : APPLICANT: CERIANI, ROBERTO L.
 : APPLICANT: PETERSON, JERRY A.
 : TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
 : TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
 : TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
 : NUMBER OF SEQUENCES: 81
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: MORRISON & FOERSTER
 : STREET: 755 Page Mill Road
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94304-1018
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/525,539A
 : FILING DATE: 14-SEP-1995
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: DYLAN, TYLER
 : REGISTRATION NUMBER: 37,612
 : REFERENCE/DOCKET NUMBER: 27633-20001.21
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 813-5600
 : TELEFAX: (415) 494-0792
 : TELEX: 706141
 : INFORMATION FOR SEQ ID NO: 76:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 117 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 US-08-525-539A-76

RESULT 13
 US-08-525-539A-47
 : Sequence 47, Application US/08525539A
 : Patent No. 6309636
 : GENERAL INFORMATION:
 : APPLICANT: DO COUTO, FERNANDO J.R.
 : APPLICANT: CERIANI, ROBERTO L.
 : APPLICANT: PETERSON, JERRY A.
 : TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
 : TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE
 : TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
 : NUMBER OF SEQUENCES: 81
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: MORRISON & FOERSTER
 : STREET: 755 Page Mill Road
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94304-1018
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/525,539A
 : FILING DATE: 14-SEP-1995
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: DYLAN, TYLER
 : REGISTRATION NUMBER: 37,612
 : REFERENCE/DOCKET NUMBER: 27633-20001.21
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 813-5600
 : TELEFAX: (415) 494-0792
 : TELEX: 706141
 : INFORMATION FOR SEQ ID NO: 47:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 136 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 US-08-525-539A-47

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;      ;
;      ;   Single
;      ;   TOPOLOGY: linear
US-08-525-539A-76

Query Match          80.1% ; Score 496; DB 4; Length 117;
Best Local Similarity 78.6%; Pred. No. 1.2e-41;
Matches 92; Conservative 11; Mismatches 12; Indels 2; Gaps 1

QY    1 EVOLQQSGPELVKPGTSVRIKCTSGYTFTETTHWVKQSHGKSLEWIGNPNNGTTY 60
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Db     1 EVOLQQSGPELVKPGASKMKISCEASGSYFTGYTHWVKQSHGMLEWLGINPYNGTVY 60
      |||||

QY    61 NQPFEDKATLTVDKSSSTAYMELSLTSSEDSAVIYCAGWNF--DYWGQGTTTLTVSS 115
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Db     61 NQAFQDKATLTVDKSSGTAYMELLSTSEDSAVIFYCARRWRITMDYWGGGTSVTVSS 117
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; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -19..-1
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN
; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
; FEATURE:
; NAME/KEY: domain
; LOCATION: 31..35
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
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; NAME/KEY: domain
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; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
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; NAME/KEY: domain
; LOCATION: 99..109
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
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US-08-116-778E-1

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Query Match          79.9%; Score 494.5; DB 2; Length 139;
Best Local Similarity 79.2%; Pred. No. 2.le-41;
Matches 95; Conservative 7; Mismatches 13; Indels 5; Gaps 1;

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Db 20 EVQLQQSGPELVKPGASVKISCKASGYTFDYNMDVKQSHGKSLGWIGYIPNNGGTG 79
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Qy 61 NQKFDKATLVDKSSSTAYMELSLTSEDSAVYYCA-----CWPNFDYWGQGTTLTVSS 115
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RESULT 15
US-08-438-562-1
; Sequence 1, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:

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; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUNANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
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; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
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; NAME/KEY: domain
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; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
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; NAME/KEY: domain
; LOCATION: 50..66
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; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 99..109
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
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US-08-438-562-1

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Query Match          79.9%; Score 494.5; DB 2; Length 139;
Best Local Similarity 79.2%; Pred. No. 2.le-41;
Matches 95; Conservative 7; Mismatches 13; Indels 5; Gaps 1;

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Qy 1 EVOLQSGPELVKPGTSYRISCKTSGYTFTEYTIHWVKQSHKSLWIGNINPNNGGTTY 60
Db 20 EVOLQSGPELVKPGTSYRISCKTSGYTFTEYTIHWVKQSHKSLWIGNINPNNGGTTY 79
Qy 61 NOKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAA-----GNFDYWGQGTTLTVSS 115
Db 80 NOKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCATYGHYYGYMFAYWGQGTTLTVSSA 139

Search completed: July 21, 2003, 13:32:25
Job time : 13.4324 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2003, 13:20:30 ; Search time 11.5676 Seconds
(without alignments)
272.162 Million cell updates/sec

Title: US-09-929-546-19

Perfect score: 569

Sequence: 1 DIVTOSHKPMSTSVGDRVS.....COQNSYPLTFGAGTMLDLK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	569	100.0	107	3	US-08-838-682-19
2	569	100.0	107	4	US-08-895-914-19
3	569	100.0	107	4	US-09-357-710A-19
4	521	91.6	107	4	US-09-406-535-4
5	513	90.2	107	1	US-07-634-278-50
6	513	90.2	107	1	US-08-477-728-50
7	513	90.2	107	1	US-08-474-040-50
8	513	90.2	107	1	US-08-487-200-50
9	513	90.2	107	4	US-08-484-537-50
10	504	88.6	107	1	US-08-491-845-4
11	472	83.0	249	2	US-08-797-689-18
12	471	82.8	107	3	US-08-767-128-32
13	471	82.8	127	4	US-08-646-265A-27
14	468	82.2	147	2	US-08-653-402B-4
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17	467	82.1	123	1	US-08-398-611A-20
18	467	82.1	123	2	US-08-491-334A-20
19	467	82.1	123	3	US-09-027-449-17
20	467	82.1	123	3	US-08-804-444A-17
21	467	82.1	123	4	US-09-026-985-17
22	467	82.1	123	4	US-09-121-952A-17
23	467	82.1	123	4	US-09-234-340A-17
24	466	81.9	108	4	US-08-752-693A-1
25	466	81.9	132	1	US-08-253-877C-55
26	466	81.9	132	2	US-08-452-164A-55
27	466	81.9	132	4	US-08-976-183A-36

28 466 81.9 132 4 US-08-976-183A-37 Sequence 37, Appl
29 465.5 81.8 110 1 US-08-497-312-23 Sequence 23, Appl
30 465 81.7 237 2 US-08-224-591-16 Sequence 16, Appl
31 465 81.7 237 2 US-08-926-789-16 Sequence 16, Appl
32 465 81.7 241 2 US-08-224-591-18 Sequence 18, Appl
33 465 81.7 241 2 US-08-926-789-18 Sequence 18, Appl
34 465 81.7 245 4 US-09-069-821-5 Sequence 5, Appl
35 465 81.7 265 4 US-09-420-592A-5 Sequence 5, Appl
36 464.5 81.6 108 2 US-08-657-012-25 Sequence 25, Appl
37 464.5 81.6 108 3 US-09-013-872-25 Sequence 25, Appl
38 464.5 81.6 108 4 US-09-184-198-25 Sequence 25, Appl
39 464.5 81.6 108 4 US-09-633-653-25 Sequence 25, Appl
40 464 81.5 237 1 US-08-398-612A-28 Sequence 28, Appl
41 464 81.5 237 1 US-08-398-611A-28 Sequence 28, Appl
42 464 81.5 237 2 US-08-491-334A-28 Sequence 28, Appl
43 464 81.5 237 3 US-09-027-449-25 Sequence 25, Appl
44 464 81.5 237 3 US-08-804-444A-25 Sequence 25, Appl
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ALIGNMENTS

RESULT 1
US-08-838-682-19
; Sequence 19, Application US/08838682
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neill H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-682-19

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Best Local Similarity 100.0%; Pred. No. 1.5e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 RFTGSGSGTDFLTITNVQSEDLADYFCQOQYNSYPLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDFLTITNVQSEDLADYFCQOQYNSYPLTFGAGTMDLKL 107

RESULT 2

US-08-895-914-19
Sequence 19, Application US/08895914
Patent No. 6136311
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603-1051
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,914
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,682
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1173
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-895-914-19

Query Match 100.0%; Score 569; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 RFTGSGSGTDFLTITNVQSEDLADYFCQOQYNSYPLTFGAGTMDLKL 107

RESULT 3

US-09-357-710A-19
Sequence 19, Application US/09357710A
Patent No. 6290956
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: Lois M. Kwagiroch; B2L 242/025
CURRENT APPLICATION NUMBER: US/09/357,710A
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 107
TYPE: PRT
ORGANISM: Mus sp.
US-09-357-710A-19

Query Match 100.0%; Score 569; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 RFTGSGSGTDFLTITNVQSEDLADYFCQOQYNSYPLTFGAGTMDLKL 107

RESULT 4

US-09-406-535-4
Sequence 4, Application US/09406535
Patent No. 6376653
GENERAL INFORMATION:
APPLICANT: Connie L. Erickson-Miller
APPLICANT: Stephen D. Holmes
APPLICANT: James D. Winkler
TITLE OF INVENTION: Tie2 Antagonist Antibodies
FILE REFERENCE: P50844
CURRENT APPLICATION NUMBER: US/09/406,535
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: 60/102,100
PRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
ORGANISM: Mus musculus
US-09-406-535-4

Query Match 91.6%; Score 521; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 1.1e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Db 61 RFTGSGSGTDFLTITNVQSEDLADYFCQOQYNSYPLTFGAGTMDLKL 107

RESULT 5
US-07-634-278-50

Sequence 50, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-50

Query Match 90.2%; Score 513; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.8e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Db 1 DIVMTQSHKFMSTSVGDRVSTICKASQDVGSAVVVHQQKSGQSPKLLIYWASTRHTGVPD 60

Qy 61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYSIFPLTFGAGTRLEKL 107

RESULT 6
US-08-477-728-50
Sequence 50, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-50

Query Match 90.2%; Score 513; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.8e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIVMTQSHKFMSTSVGDRVSTICKASQDVGTAVDWYQKPCQSPKLLIYWASTRHTGVPD 60
Db 1 DIVMTQSHKFMSTSVGDRVSTICKASQDVGSAVVVHQQKSGQSPKLLIYWASTRHTGVPD 60

Qy 61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYSIFPLTFGAGTRLEKL 107

RESULT 7
US-08-474-040-50
Sequence 50, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-50

Query Match 90.2%; Score 513; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.8e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIWVTQSHKFMSTSVGDRVSIICKASQDVGTAYDWTQQKPGQSPKLLIYWASTRHTGVPD 60
DB 1 DIWVTQSHKFMSTSVGDRVSIICKASQDVGTAYDWTQQKPGQSPKLLIYWASTRHTGVPD 60
QY 61 RFTGSGSGDTFTLTITNVQSEDLDYFCQYNSYPLTFGAGTMDLK 107
DB 61 RFTGSGSGDTFTLTITNVQSEDLDYFCQYNSYPLTFGAGTMDLK 107

RESULT 8
US-08-487-200-50
Sequence 50, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California

COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-50

Query Match 90.2%; Score 513; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.8e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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DB 1 DIWVTQSHKFMSTSVGDRVSIICKASQDVGTAYDWTQQKPGQSPKLLIYWASTRHTGVPD 60
QY 61 RFTGSGSGDTFTLTITNVQSEDLDYFCQYNSYPLTFGAGTMDLK 107
DB 61 RFTGSGSGDTFTLTITNVQSEDLDYFCQYNSYPLTFGAGTMDLK 107

RESULT 9
US-08-484-537-50
Sequence 50, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US/07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA: US/07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-537-50

Query Match 90.2%; Score 513; DB 4; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.8e-45;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIVTQSHKPMSTSVGDRVSIICKASODVCTAVDWYQOKPGQSPKLLIYWASTRHTGVDP 60
Db 1 DIVTQSHKPMSTSVGDRVSIICKASODVGVAVVHHQKSGQSPKLLIYWASTRHTGVDP 60
QY 61 RFTGSGSGTDTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDTLTITNVQSEDLADYFCQQYSIFPLTFGAGTMDLKL 107

RESULT 10
US-08-491-845-4
; Sequence 4, Application US/08491845
; Patent No. 5773247
; GENERAL INFORMATION:
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: KINACHI, Kazuhiko
; APPLICANT: ED, Yasuyuki
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00039
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MAEDA-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-491-845-4
Query Match 88.6%; Score 504; DB 1; Length 107;
Best Local Similarity 88.8%; Pred. No. 5.5e-44;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIVTQSHKPMSTSVGDRVSIICKASODVCTAVDWYQOKPGQSPKLLIYWASTRHTGVDP 60
Db 1 DIVTQSHKPMSTSVGDRVSIICKASODVGVADVAVYQOKPGQSPKLLIYWASTRHTGVDP 60
QY 61 RFTGSGSGTDTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDTLTITNVQSEDLADYFCQQYSFPLTFGAGTMDLKL 107

RESULT 11
US-08-797-689-18
; Sequence 18, Application US/08797689
; Patent No. 5876969
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guittion, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:32:31 ; Search time 32.2928 Seconds
(without alignments)
393.503 Million cell updates/sec

Title: us-09-929-546-19

Perfect score: 569

Sequence: 1 DIVMTQSHKFMSTSVGDRVS.....COQYNSYPLTFGAGTMDLKL 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PublishedApplications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep1.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep2.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep3.*
- 13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	569	100.0	107	12	US-09-929-665-19
2	569	100.0	107	12	US-09-929-546-19
3	476	83.7	107	12	US-09-874-141-9
4	476	83.7	133	12	US-09-874-141-51
5	472	83.0	249	11	US-09-984-186-18
6	472	83.0	249	15	US-10-237-667-18
7	472	83.0	249	15	US-10-237-708-18
8	472	83.0	249	15	US-10-237-866-18
9	472	83.0	249	15	US-10-237-871-18
10	472	83.0	249	15	US-10-237-624-18
11	471	82.8	127	12	US-09-749-873-27
12	471	82.8	333	15	US-10-059-261-61
13	469	82.4	331	15	US-10-059-261-169
14	467	82.1	123	12	US-09-726-258-17
15	465	81.7	240	15	US-10-096-246-36
16	465	81.7	245	11	US-09-956-086-5

ALIGNMENTS

RESULT 1

US-09-929-665-19
; Sequence 19, Application US/09929665
; Publication No. US20030003101A1
; GENERAL INFORMATION:
; APPLICANT: Bandner, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: B2L 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-19

Query Match 100.0%; Score 569; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.1e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQOKPGQSPKLLIYWASTRHTGVPD 60

Qy 61 RFTGSGSGTDFTLITNNVQSEDLADYFCQQYNSYPLTFGAGTMDLKL 107
|||||

Db 61 RFTGSGSGTDFTLITNNVQSEDLADYFCQQYNSYPLTFGAGTMDLKL 107
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Sequence 5, Appli
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Sequence 5, Appli
Sequence 25, Appli
Sequence 4, Appli
Sequence 37, Appli
Sequence 35, Appli
Sequence 59, Appli
Sequence 5, Appli
Sequence 36, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 104, App
Sequence 104, App
Sequence 32, Appli
Sequence 2, Appli
Sequence 130, App
Sequence 104, App
Sequence 2, Appli
Sequence 104, App
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 13, Appli
Sequence 134, App

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RESULT 2
US-09-929-546-19
; Sequence 19, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bandet, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-546-19

Query Match      100.0%; Score 569; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.1e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDMYQKPGSPKLLIYWASTRHTGVPD 60
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Db 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDMYQKPGSPKLLIYWASTRHTGVPD 60
    |||||||
QY 61 RTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPLTFCAGTMLDLK 107
    |||||||
Db 61 RTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPLTFCAGTMLDLK 107
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RESULT 3
US-09-874-141-9
; Sequence 9, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized peptide
US-09-874-141-9

Query Match      83.7%; Score 476; DB 12; Length 107;
Best Local Similarity 85.0%; Pred. No. 5e-40;
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Db 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDMYQKPGSPKLLIYWASTRHTGVPD 60
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QY 61 RTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPLTFCAGTMLDLK 107
    |||||||
Db 61 RTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPLTFCAGTMLDLK 107
    |||||||

RESULT 4
US-09-874-141-51
; Sequence 51, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-141-51

Query Match      83.7%; Score 476; DB 12; Length 133;
Best Local Similarity 85.0%; Pred. No. 6.4e-40;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDMYQKPGSPKLLIYWASTRHTGVPD 60
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Db 25 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDMYQKPGSPKLLIYSASNRYTGVPD 84
    |||||||
QY 61 RTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPLTFCAGTMLDLK 107
    |||||||
Db 85 RTGSGSGTDFLTITNVQSEDLADYFCQOYNSYPTTFGGGKLEIK 131
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RESULT 5
US-09-984-186-18
; Sequence 18, Application US/09984186
; Patent No. US20020151011A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,186
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1  APPLICATION NUMBER: US 08/256,927
2  FILING DATE: 28-JUL-1994
3  APPLICATION NUMBER: FR 92/01064
4  FILING DATE: 31-JAN-1992
5  APPLICATION NUMBER: PCT/FR93/00085
6  FILING DATE: 28-JAN-1993
7  ATTORNEY/AGENT INFORMATION:
8  NAME: Smith Ph.D., Julie K.
9  REGISTRATION NUMBER: P-38,619
10 REFERENCE/DOCKET NUMBER: ST92006-US
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: (610) 454-3839
13 TELEFAX: (610) 454-3808
14 INFORMATION FOR SEQ ID NO: 18:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 249 amino acids
17 TYPE: amino acid
18 TOPOLOGY: linear
19 MOLECULE TYPE: protein
20 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
21
22 US-10-237-667-18
23
24 Query Match 83.0%; Score 472; DB 15; Length 249;
25 Best Local Similarity 83.2%; Pred. No. 3.le-39;
26 Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
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29 Db 143 NQLTQSPNSMSTVSGDVRVSTCKASQDVDTSVANYQOKPGQSPKLLIYWASTRTGTGVPD 202
30
31 QY 61 RTGSGSGTDFTLITINVOSEDLADYFCQQYNSYPLTFGAGTMDLTK 107
32 Db 203 RTGSGSGTDFTLITINSQSESDADYFCQQYSSYPWTFGGKTKLEIK 249
33
34 RESULT 7
35 US-10-237-708-18
36 ; Sequence 18, Application US/10237708
37 ; Publication No. US20030036170A1
38 ; GENERAL INFORMATION:
39 ; APPLICANT: Fleer, Reinhard
40 ; Fournier, Alain
41 ; Guillon, Jean-Dominique
42 ; Jung, Gerard
43 ; Yeh, Patrice
44 ; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, COMPOSITION
45 ; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
46 ; CONTAINING SAID POLYPEPTIDES
47
48 NUMBER OF SEQUENCES: 36
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: Rhone-Poulenc Rorer Inc.
51 STREET: 500 Arcola Road, 3C43
52 CITY: Collegeville
53 STATE: PA
54 COUNTRY: USA
55 ZIP: 19426
56
57 COMPUTER READABLE FORM:
58 MEDIUM TYPE: Floppy disk
59 COMPUTER: Macintosh
60 OPERATING SYSTEM: System 7.1
61 SOFTWARE: Word 5.1 (PatentIn)
62
63 CURRENT APPLICATION DATA:
64 APPLICATION NUMBER: US/10/237,708
65 FILING DATE: 10-Sep-2002
66 CLASSIFICATION: <Unknown>
67
68 PRIOR APPLICATION DATA:
69 APPLICATION NUMBER: US/08/797,689
70 FILING DATE: 31-JAN-1997
71 APPLICATION NUMBER: US 08/256,927
72 FILING DATE: 28-JUL-1994
73 APPLICATION NUMBER: FR 92/01064
74 FILING DATE: 31-JAN-1992
75 APPLICATION NUMBER: PCT/FR93/00085

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Db 81 RFTGSGGTDTLTTITNQSEDLADYFCQOYNSYPRAFGGTKLEIK 127
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RESULT 12
US-10-059-261-169
; Sequence 61, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; FILE REFERENCE: (PTPC)
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector pAcgp67-ScFv461
; OTHER INFORMATION: peptide sequence
US-10-059-261-169

Query Match 82.8%; Score 471; DB 15; Length 333;
Best Local Similarity 84.1%; Pred. No. 5,4e-39;
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
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Db 221 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGSPKLLIYWASTRHTGVPD 280
QY 61 RFTGSGGTDTLTTITNQSEDLADYFCQOYNSYPLTFGAGTMDLK 107
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Db 281 RFTGSGGTDTLTTITNQSEDLADYFCQOYNSYPLTFGAGTMDLK 327

RESULT 13
US-10-059-261-169
; Sequence 169, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; FILE REFERENCE: (PTPC)
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector pAcgp67-ScFv350
; OTHER INFORMATION: peptide sequence
US-10-059-261-169

Query Match 82.4%; Score 469; DB 15; Length 331;
Best Local Similarity 83.2%; Pred. No. 8,4e-39;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGSPKLLIYWASTRHTGVPD 60
|||||
Db 219 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGSPKLLIYWASTRHTGVPD .278
QY 61 RFTGSGGTDTLTTITNQSEDLADYFCQOYNSYPLTFGAGTMDLK 107
|||||
Db 279 RFTGSGGTDTLTTITNQSEDLADYFCQOYNSYPLTFGAGTMDLK 325

RESULT 14
US-09-726-258-17
; Sequence 17, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsai, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokhi, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-726-258-17

Query Match 82.1%; Score 467; DB 12; Length 123;
Best Local Similarity 83.2%; Pred. No. 4,6e-39;
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGSPKLLIYWASTRHTGVPD 60
|||||
Db 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGSPKLLIYWASTRHTGVPD 60
QY 61 RFTGSGGTDTLTTITNQSEDLADYFCQOYNSYPLTFGAGTMDLK 107
|||||

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Db      61  RFTGSGSGDTFTLTISHVQSEDLADYFCQOYNIYPLTFTGPGTKLEK 107

RESULT 15
US-10-096-246-36
; Sequence 36, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
; FILE REFERENCE: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; CURRENT APPLICATION NUMBER: US/10/096,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-36

Query Match      81.7%; Score 465; DB 15; Length 240;
Best Local Similarity 78.5%; Pred. No. 1.5e-38;
Matches 84; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY      1  DIVWTQSHKFMSTSVGDRVSIICKASQDVGTAVDWTQOKPGQSPKLLIYWASTRHTGVPD 60
Db      133  DIELTQSPNSLSTSIGDRIRITCKASQDDVDVAVGWYQQRPGQSPKLLIFWSSTRHTGVPD 192

QY      61  RFTGSGSGDTFTLTITNVQSEDLADYFCQOYNSYPLTFEGAGTMLDLK 107
Db      193  RFTGSGSGDTFTLTISNVQSEDLADYFCHOYSSYPTFTGSGTKLEIK 239

Search completed: July 21, 2003, 13:46:34
Job time : 33.2928 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:23:15 ; Search time 23.6171 seconds
(without alignments)
435.548 Million cell updates/sec

Title: US-09-929-546-19
Perfect score: 569
Sequence: 1 DIVMTQSHKFMSTVSGDRVS.....COQYNSYPLTFGAGTMLDLK 107
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	526	92.4	117	2 S42466	Ig kappa chain V r
2	499	87.7	131	2 PL0207	anti-idiotypic ant
3	483	84.9	152	2 S30751	Ig kappa chain pre
4	482	81.2	107	2 A28195	Ig kappa chain V r
5	462	81.2	108	2 PL0204	anti-DNA autoantib
6	452	79.4	107	2 B28195	Ig kappa chain V r
7	452	79.4	107	2 S32192	Ig kappa chain V r
8	450	79.1	107	2 S32191	Ig kappa chain V r
9	446	78.4	149	1 KVM511	Ig kappa chain pre
10	444.5	78.1	108	2 B44371	Ig kappa chain V r
11	440	77.3	119	2 PQ0265	Ig kappa chain V r
12	436	76.6	128	2 A47159	Ig kappa chain V r
13	434	76.3	98	2 PH1072	Ig lambda chain V
14	432	75.9	100	2 H38601	Ig light chain V r
15	433	74.3	107	2 S09967	Ig kappa chain V-J
16	416.5	73.2	108	2 PL0083	Ig kappa chain pre
17	416	73.1	90	2 S38561	Ig light chain V r
18	416	73.1	94	2 F33730	Ig light chain V r
19	408	71.7	93	2 S38559	Ig kappa chain V r
20	405	71.2	127	2 S04577	Ig light chain V r
21	401	70.5	98	2 PH1073	Ig kappa chain pre
22	400	70.3	107	2 S38713	Ig light chain V r
23	394	69.2	90	2 I38601	Ig kappa chain V r
24	394	69.2	136	1 KVM521	Ig kappa chain pre
25	393.5	69.2	106	2 PL0088	Ig kappa chain V r
26	393	69.1	111	2 D37266	Ig kappa chain V r
27	393	69.1	145	2 PL0014	Ig kappa chain pre
28	387.5	68.1	225	2 S37484	Ig kappa chain - m
29	384	67.5	113	2 A49260	antitumor monoclon

30	383	67.3	113	2 PL0263	Ig kappa chain V r
31	381	67.0	107	2 S36264	Ig lambda chain V
32	381	67.0	134	2 PC1214	Ig kappa chain pre
33	379.5	66.7	138	2 S26040	Ig kappa chain pre
34	379	66.6	107	2 D53285	Ig kappa chain V a
35	379	66.6	107	2 S36268	Ig lambda chain V
36	378	66.4	107	2 S33132	Ig kappa chain V r
37	377	66.3	108	2 S19674	Ig kappa chain V r
38	376.5	66.2	118	2 PT0356	Ig kappa chain V r
39	376	66.1	132	2 S40334	Ig kappa chain - h
40	375	65.9	108	1 K1H0LY	Ig kappa chain V-I
41	374	65.7	82	2 S38560	Ig light chain V r
42	374	65.7	214	2 S68212	Ig kappa chain (Ma
43	373.5	65.6	112	2 S09970	Ig kappa chain V-J
44	372	65.4	88	2 A37262	Ig kappa chain V r
45	372	65.4	112	2 F30538	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S42466
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42466
R:Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
Submitted to the EMBL Data Library, March 1994
A:Reference number: S42466
A:Accession: S42466
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <SH1>
A:Cross-references: EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID:g460825
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 526; DB 2; Length 117;
Best Local Similarity 91.6%; Pred. No. 5.7e-42;
Matches 98; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY	1	DIVMTQSHKFMSTVSGDRVSIICKASQDVGTAVDVTQKPGQSPKLLIYWASTRHGVPD 60
DB	11	DIVMTQSHKFMSTVSGDRVSIICKASQDVGTAVDVTQKPGQSPKLLIYWASTRHGVPD 70
QY	61	RFTGSGSGTDFLTITINVSQEDLADYFCQOYSYPLTFGAGTMLDLK 107
DB	71	RFTGSGSGTDFLTITINVSQEDLADYFCQOYSYPLTFGAGTMLDLK 117

RESULT 2

PL0207
anti-idiotypic antibody E225, kappa chain V region precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PL0207
R:Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
Mol. Immunol. 27, 429-433, 1990
A:Title: Nucleotide sequence of the VH, VL regions of an anti-idiotopic antibody reas
A:Reference number: PL0207; MUID:90309764; PMID:1973259
A:Accession: PL0207
A:Molecule type: mRNA
A:Residues: 1-131 <SOU>
A:Note: This sequence corresponds to subgroup V mouse immunoglobulin light chain
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-20/Domain: signal sequence #status predicted <SIG>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-117/Region: complementarity-determining 3
F:116-127/Region: J region

Query Match 87.7%; Score 499; DB 2; Length 131;
Best Local Similarity 87.9%; Pred. No. 2.1e-39;
Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||
Db 21 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 80
|||||

Qy 61 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 107
|||||

Db 81 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 127
|||||

RESULT 3
S30751

Ig kappa chain precursor V region - mouse
A:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C:Accession: S30751
R:Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
Nucleic Acids Res. 15, 5496, 1987
A:Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
A:Reference number: S30751; MUID:87260030; PMID:3601683
A:Accession: S30751
A:Molecule type: mRNA
A:Residues: 1-152 <GRA>
A:Cross-references: EMBL:X05877; NID:g52195; PIDN:CAA29301.1; PID:g52196
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:45-119/Domain: immunoglobulin homology <IMM>
F:138-152/Domain: C region (C-kappa) (fragment) #status predicted <CRE>

Query Match 84.9%; Score 483; DB 2; Length 152;
Best Local Similarity 85.0%; Pred. No. 7.4e-38;
Matches 91; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||
Db 30 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 89
|||||

Qy 61 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 107
|||||

Db 90 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 136
|||||

RESULT 4
A28195

Ig kappa chain V region (anti-haloperidol antibody A) - mouse
A:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000
C:Accession: A28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: A28195
A:Molecule type: mRNA
A:Residues: 1-107 <SHE>
A:Cross-references: GB:M19766; NID:g197039; PIDN:AAA38891.1; PID:g197040
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 462; DB 2; Length 107;
Best Local Similarity 81.3%; Pred. No. 4.5e-36;
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||
Db 1 DILMTQSQKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||

Qy 61 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 107
|||||

|||||
Db 61 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 107
|||||

RESULT 5
PL0204

anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
A:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PL0204
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies fro
A:Reference number: PL0198; MUID:90309768; PMID:2114528
A:Accession: PL0204
A:Molecule type: mRNA
A:Residues: 1-108 <SMI>
A:Cross-references: GB:X53644; NID:g50198; PIDN:CAA37695.1; PID:g930144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:50-56/Region: complementarity-determining 2
F:89-97/Region: complementarity-determining 3
F:96-108/Region: JH region

Query Match 81.2%; Score 462; DB 2; Length 108;
Best Local Similarity 81.3%; Pred. No. 4.5e-36;
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||
Db 1 DIVMTQSQKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||

Qy 61 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 107
|||||

Db 61 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 107
|||||

RESULT 6
B28195

Ig kappa chain V region (anti-haloperidol antibody B) - mouse
A:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000
C:Accession: B28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino aci
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: B28195
A:Molecule type: mRNA
A:Residues: 1-107 <SHE>
A:Cross-references: EMBL:M19767; NID:g197041; PIDN:AAA38892.1; PID:g197042
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 452; DB 2; Length 107;
Best Local Similarity 79.4%; Pred. No. 3.8e-35;
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||
Db 1 DILMTQSQKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
|||||

Qy 61 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 107
|||||

Db 61 RFTGSGGTDFTLTITNVQSEDADYFCQQYNSYPYTFGGTGMLEIK 107
|||||

RESULT 7
S32192

Ig kappa chain V region - mouse (fragment)
A:Species: Mus musculus (house mouse)

R;Rabbltts, T.H.; Hamlyn, P.H.; Matthyssens, G.; Roe, B.A.

P00265

Ig kappa chain V region (NC1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: P00265
R:Lothman, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 105, 283-284, 1991
A:Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal
A:Reference number: P00265; MUID:92039046; PMID:1937027
A:Accession: P00265
A:Molecule type: mRNA
A:Residues: 1-119 <LOH>
A:CROSS-references: GB:M59985
C:Comment: This protein recognizes a restricted idiotype associated with antibodies spec
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:28-102/Domain: immunoglobulin homology <IMM>
F:36-46/Region: complementarity-determining 1
F:62-68/Region: complementarity-determining 2
F:101-109/Region: complementarity-determining 3

Query Match 77.3%; Score 440; DB 2; Length 119;
Best Local Similarity 79.4%; Pred. No. 5.5e-34;
Matches 85; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTVSGDRVSIICKASQDVGTAVDNYQKPGQSPKLLIYWASTRHTGVPD 60
DB 13 DIVMTQSHKFMSTVSGDRVSIICKASQDVSTVAVNYQKPGQSPKLLIYSASYRTGVPD 72
QY 61 RFTGSGSGTDTFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLK 107
DB 73 RFTGSGSGTDTFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLK 119

RESULT 12

Ig lambda chain V region (CEA-specific mard r84.66) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A47159
R:Galda, F.J.; Pleper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.
J. Biol. Chem. 268, 14138-14145, 1993
A:Title: Molecular characterization of a cloned idiotypic cascade containing a network a
A:Reference number: A47159; MUID:93300804; PMID:7686150
A:Accession: A47159
A>Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-128 <GAI>
A:Experimental source: hybridoma 666.C4
A:Note: sequence extracted from NCBI backbone (NCBIN:134419, NCBIIP:134420)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 436; DB 2; Length 128;
Best Local Similarity 77.6%; Pred. No. 1.4e-33;
Matches 83; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTVSGDRVSIICKASQDVGTAVDNYQKPGQSPKLLIYWASTRHTGVPD 60
DB 21 DIVMTQSHKFMSTVSGDRVSIICKASQDVSTVAVNYQKPGQSPKLLIYSASYRTGVPD 80
QY 61 RFTGSGSGTDTFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLK 107
DB 81 RFTGSGSGTDTFTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLK 127

RESULT 13

Ig light chain V region (clone 83-cl) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1072

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1072

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-98 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 434; DB 2; Length 98;
Best Local Similarity 83.7%; Pred. No. 1.6e-33;
Matches 82; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTVSGDRVSIICKASQDVGTAVDNYQKPGQSPKLLIYWASTRHTGVPD 60
DB 1 DIVMTQSHKFMSTVSGDRVSIICKASQDVSTVAVNYQKPGQSPKLLIYSASYRTGVPD 60

QY 61 RFTGSGSGTDTFTLTITNVQSEDLADYFCQOYNSYPLTF 98

DB 61 RFTGSGSGTDTFTLTITNVQSEDLADYFCQOYNSYPLTF 98

RESULT 14

Ig kappa chain V region (3A3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: H38601
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Reference number: A38601; MUID:91115823; PMID:1709527
A:Accession: H38601
A:Molecule type: mRNA
A:Residues: 1-100 <GOS>
A:CROSS-references: GB:M57985; NID:9196416; PIDN:AAA53366.1; PID:9196417
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-82/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 432; DB 2; Length 100;
Best Local Similarity 81.8%; Pred. No. 2.5e-33;
Matches 81; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 9 KPMSTVSGDRVSIICKASQDVGTAVDNYQKPGQSPKLLIYWASTRHTGVPDRFTGSGG 68
DB 1 KPMSTVSGDRVSIICKASQDVGTAVDNYQKPGQSPKLLIYSASYRTGVPDRFTGSGG 60

QY 69 TDTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLK 107

DB 61 TDTLTITNVQSEDLADYFCQOYNSYPLTFGAGTMDLK 99

RESULT 15

Ig kappa chain V-J region (31-9D) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Aug-1996
C:Accession: S09967
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibo
A:Reference number: S09967; MUID:90269328; PMID:2347362
A:Accession: S09967
A:Molecule type: mRNA
A:Residues: 1-107 <REI>
A:CROSS-references: EMBL:X51855
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; Immunoglobulin

```

Query Match      74.3%; Score 423; DB 2; Length 107;
Best Local Similarity 77.6%; Pred. No. 1.9e-32;
Matches 83; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy      1 DIVMTQSHKFMSTSVGDRVSIICKASODVGTAVDWYQQKPGQSPKLLIYWASTRHTGVPD 60
        ||||| ||||| || || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      1 DIVMTQSHKFMSTSVXDRDSITCKASODVNTAVAVYQQKPGQSPKLLICSASSRYTGVPD 60

Qy      61 RFTGSGGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMLDLK 107
        ||||| ||||| || | :||| :||| | ||| | ||| | ||| | ||| |
Db      61 RFTGSGGTDFTLTINTVHAEDLAVYCCQYYSRPXTFGXGTXK 107

```

Search completed: July 21, 2003, 13:33:22
Job time : 24.6171 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:11:26 ; Search time 12.5315 Seconds
(without alignments)
354.144 Million cell updates/sec

Title: US-09-929-546-19
Perfect score: 569
Sequence: 1 DIVMTQSHKFMSTVSGDRVS.....COQYNSYPLTFGAGTMDLKD 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	446	78.4	149	1 KV5A_MOUSE	P01633 mus musculus
2	394	69.2	136	1 KV5B_MOUSE	P01634 mus musculus
3	375	65.9	108	1 KV1M_HUMAN	P01605 homo sapien
4	375	65.9	108	1 KV1Y_HUMAN	P80362 homo sapien
5	368	64.7	134	1 KV4C_HUMAN	P06314 homo sapien
6	367	64.5	114	1 KV4A_HUMAN	P01625 homo sapien
7	363	63.8	108	1 KV1Q_HUMAN	P01609 homo sapien
8	362	63.6	108	1 KV1P_HUMAN	P01608 homo sapien
9	360.5	63.4	133	1 KV4B_HUMAN	P06313 homo sapien
10	358	62.9	108	1 KV1V_HUMAN	P04430 homo sapien
11	356	62.6	108	1 KV1L_HUMAN	P01604 homo sapien
12	356	62.6	108	1 KV1S_HUMAN	P01611 homo sapien
13	353	62.0	114	1 KV1A_MOUSE	P01632 mus musculus
14	352	61.9	108	1 KV5K_MOUSE	P01644 mus musculus
15	349.5	61.4	129	1 KV3H_HUMAN	P04207 homo sapien
16	349	61.3	108	1 KV1K_HUMAN	P01603 homo sapien
17	348	61.2	108	1 KV1Q_HUMAN	P01607 homo sapien
18	347	61.0	108	1 KV5J_MOUSE	P01643 mus musculus
19	347	61.0	108	1 KV5L_MOUSE	P01645 mus musculus
20	344	60.5	108	1 KV1A_HUMAN	P01593 homo sapien
21	344	60.5	108	1 KV1G_HUMAN	P01599 homo sapien
22	343.5	60.4	107	1 KV1D_HUMAN	P01596 homo sapien
23	343.5	60.4	109	1 KV1D_HUMAN	P01622 homo sapien
24	343	60.3	108	1 KV1B_HUMAN	P01594 homo sapien
25	343	60.3	108	1 KV5N_MOUSE	P01647 mus musculus
26	342.5	60.2	109	1 KV3F_HUMAN	P01624 homo sapien
27	342	60.1	108	1 KV1F_HUMAN	P01598 homo sapien
28	342	60.1	108	1 KV5M_MOUSE	P01646 mus musculus
29	342	60.1	108	1 KV5Q_MOUSE	P01648 mus musculus
30	341	59.9	108	1 KV1R_HUMAN	P01610 homo sapien
31	340.5	59.8	129	1 KV3L_HUMAN	P81335 homo sapien
32	339	59.6	108	1 KV5P_MOUSE	P01649 mus musculus
33	339	59.6	129	1 KV1W_HUMAN	P04431 homo sapien

RESULT 1				
KV5A_MOUSE				
ID	KV5A_MOUSE	STANDARD:	PRT;	149 AA.
AC	P01633;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DE	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	Ig kappa chain V-V region MPC11 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RX	SEQUENCE OF 1-71 FROM N.A.			
RX	MEDLINE=83001944; PubMed=6288267;			
RA	Kelley D.E., Coleclough C., Perry R.P.;			
RT	Functional significance and evolutionary development of the			
RT	5'-terminal regions of immunoglobulin variable-region genes.;			
RL	Cell 29:681-689(1982).			
RN	[2]			
RX	SEQUENCE OF 41-149 FROM N.A.			
RX	MEDLINE=80176554; PubMed=6245773;			
RA	Rabbits T.H., Hamlyn P.H., Matthysens G., Roe B.A.;			
RT	The variability, arrangement, and rearrangement of immunoglobulin			
RT	genes.;			
RL	Can. J. Biochem. 58:176-187(1980).			
RN	[3]			
RX	SEQUENCE OF 30-149.			
RX	MEDLINE=78186617; PubMed=418775;			
RA	Smith G.P.;			
RT	Sequence of the full-length immunoglobulin kappa-chain of mouse			
RT	myeloma MPC 11.;			
RL	Biochem. J. 171:337-347(1978).			
CC	-!- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS			
CC	AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE			
CC	CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL			
CC	RESIDUE OF TYPICAL KAPPA CHAINS.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: J00561; AAA38776.1; -			
DR	PIR: A01916; KVM511.			
DR	HSP: P80362; IWTLL.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_v.			
DR	Pfam: PF000047; Ig_1.			
DR	SMART: SM00406; IgV; 1.			
KW	Immunoglobulin V region; Signal; Repeat.			
FT	SIGNAL	1	29	
FT	CHAIN	30	149	IG KAPPA CHAIN V-V REGION MPC11.

P8136 homo sapien
P01620 homo sapien
P01623 homo sapien
P01666 mus musculus
P01637 mus musculus
P01595 homo sapien
P01600 homo sapien
P01606 homo sapien
P06312 homo sapien
P04946 mus musculus
P01619 homo sapien
P01671 mus musculus

```
FT DOMAIN 42 64 FRAMEWORK-1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 129 FRAMEWORK-3.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 139 148 FRAMEWORK-4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match 78.4%; Score 446; DB 1; Length 149;
Best Local Similarity 80.4%; Pred. No. 1.3e-41;
Matches 86; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTVSGDRVSIIICKASQDVGTAVDQVYQKPGQSPKLLIYWASTRTHTGVPD 60
DB 42 DIVMTQSHKFMSTVSGDRVSIIICKASQDVGTAVDQVYQKPGQSPKLLIYWASTRTHTGVPD 101
QY 61 RFTGSGSGTDTFTLTITNQVSEDLDADYFCQYNSYPLTFCAGTMDLKL 107
DB 102 RFTGSGSGTDTFTLTITNQVSEDLDADYFCQYNSYPLTFCAGTMDLKL 148

RESULT 2
KV5B_MOUSE
ID KV5B_MOUSE STANDARD; PRT; 136 AA.
AC P01634;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-V region MOPC 21 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [2]
RP SEQUENCE OF 30-136.
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00810; CAA24192.1; ALT_TERM.
DR PIR; A01917; KMS21.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 29
FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.
FT DOMAIN 30 52 FRAMEWORK-1.
FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 64 78 FRAMEWORK-2.
FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING-2.
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FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 127 136 FRAMEWORK-4.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;

Query Match 69.2%; Score 394; DB 1; Length 136;
Best Local Similarity 72.0%; Pred. No. 5.4e-36;
Matches 77; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTVSGDRVSIIICKASQDVGTAVDQVYQKPGQSPKLLIYWASTRTHTGVPD 60
DB 30 NIVMTQSPKSMNSVGERVTLTKASENVVTVSYQKPGQSPKLLIYGASNRRTGVPD 89
QY 61 RFTGSGSGTDTFTLTITNQVSEDLDADYFCQYNSYPLTFCAGTMDLKL 107
DB 90 RFTGSGSATDTFTLTITNQVSEDLDADYFCQYNSYPLTFCAGTMDLKL 136

RESULT 3
KV1M_HUMAN
ID KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapner D.G.;
RT "Complete amino acid sequence of the variable domains of two human
IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
DR PIR; A01871; K1HULY.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 65.9%; Score 375; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 4.8e-34;
Matches 69; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTVSGDRVSIIICKASQDVGTAVDQVYQKPGQSPKLLIYWASTRTHTGVPD 60
DB 1 DIQMTQSPSLSVSGDRVTITTCQASQSNVYLNWYQKPGKPLKLIYGASTREAGVPS 60
QY 61 RFTGSGSGTDTFTLTITNQVSEDLDADYFCQYNSYPLTFCAGTMDLKL 107
DB 61 RFTGSGSGTDTFTLTITNQVSEDLDADYFCQYNSYPLTFCAGTMDLKL 107
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RESULT 4
KV1Y_HUMAN
ID KV1Y_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PDB; 1WTL; 01-NOV-94.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 TN -> SD (IN REF. 2).
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 65.9%; Score 375; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 4.8e-34;
Matches 68; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 DIVMTQSHKFMSTVSGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHGTGVPD 60
DB 1 DIQMTQSPSSLSASVSGDRVTITCRASQDITNYVNWVQQRPGQAPKVLIIYGASILETGVP 60
QY 61 RFTGSGSGTDFLTITNVQSEDLADYFCQQYNSVPLTFGAGTMDLKL 107
DB 61 RFGSGSGTDFLTITNVQSEDLADYFCQQYNSVPLTFGAGTMDLKL 107

RESULT 5
KV4C_HUMAN
ID KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human v kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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DR EMBL; X02990; CAA26733.1; -.
DR PIR; A01905; K4HU17.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 64.7%; Score 368; DB 1; Length 134;
Best Local Similarity 61.1%; Pred. No. 3.6e-33;
Matches 69; Conservative 20; Mismatches 18; Indels 6; Gaps 1;

QY 1 DIVMTQSHKFMSTVSGDRVSIICKASQDVGTAVD-----WYQKPGQSPKLLIYWASTR 54
DB 21 DIVMTQSPDSLAVSLGERATINCKSSQSIYSSDNKNYLAWYQKPGQSPKLLIYWASTR 80
QY 55 HTGVPDRFTGSGSGTDFLTITNVQSEDLADYFCQQYNSVPLTFGAGTMDLKL 107
DB 81 ESGVDPDRFSGSGSGTDFLTITNVQSEDLADYFCQQYNSVPLTFGAGTMDLKL 133

RESULT 6
KV4A_HUMAN
ID KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of

```

RT subgroup IV of the kappa type (Bence-Jones protein Len).
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 RN [2]
 RP REVISION TO 9.
 RA Salomon A.;
 RL Submitted (AUG-1996) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01903; K4HULN.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 40
 FT DOMAIN 41 55
 FT DOMAIN 56 62
 FT DOMAIN 63 94
 FT DOMAIN 95 101
 FT DOMAIN 102 113
 FT DISULFID 23 94
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;
 Query Match 64.5%; Score 367; DB 1; Length 114;
 Best Local Similarity 61.9%; Pred. No. 3.8e-33;
 Matches 70; Conservative 18; Mismatches 19; Indels 6; Gaps 1;
 QY 1 DIVVTQSHKFMSTVSGDRVSIICKASQDV-----GTAVDVTQKPGSPKLLIYWASTR 54
 DB 1 DIVVTQSPDSLAVSLGERATINCKSSQVLYSSNKNLAWYQKPGQPKLLIYWASTR 60
 QY 55 HTGVDRFTGSGGDTFTLTITNQVSEDLADYFCQYNSYPLTFGAGTMDL 107
 DB 61 ESGVDRFGSGSGDTFTLTITSSLAQEDVAVYQYQYTPSYFGQGTLEIK 113
 RESULT 7
 KVIQ_HUMAN
 ID KVIQ_HUMAN STANDARD; PRT; 108 AA.
 AC P01609.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Scw.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059271; PubMed=4435756;
 RA Eullitz M., Hilschmann N.;
 RT The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides and the complete amino acid sequence.*;
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01875; KIHUSW.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DISULFID 23 49
 FT NON_TER 50 56
 SQ SEQUENCE 50 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;
 Query Match 63.6%; Score 362; DB 1; Length 108;
 Best Local Similarity 61.7%; Pred. No. 1.2e-32;
 Matches 66; Conservative 19; Mismatches 22; Indels 0; Gaps 0;
 QY 1 DIVVTQSHKFMSTVSGDRVSIICKASQDVGTAVDVTQKPGSPKLLIYWASTR 60
 DB 1 DIVVTQSPDSLAVSLGERATINCKSSQVLYSSNKNLAWYQKPGQPKLLIYWASTR 60
 QY 55 HTGVDRFTGSGGDTFTLTITNQVSEDLADYFCQYNSYPLTFGAGTMDL 107
 DB 61 ESGVDRFGSGSGDTFTLTITSSLAQEDVAVYQYQYTPSYFGQGTLEIK 113

FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;
 Query Match 63.8%; Score 363; DB 1; Length 108;
 Best Local Similarity 61.7%; Pred. No. 9.7e-33;
 Matches 66; Conservative 20; Mismatches 21; Indels 0; Gaps 0;
 QY 1 DIVVTQSHKFMSTVSGDRVSIICKASQDVGTAVDVTQKPGSPKLLIYWASTR 60
 DB 1 DIVVTQSPDSLAVSLGERATINCKSSQVLYSSNKNLAWYQKPGQPKLLIYWASTR 60
 QY 61 RFTGSGGDTFTLTITNQVSEDLADYFCQYNSYPLTFGAGTMDL 107
 DB 61 RFTGSGGDTFTLTITNQVSEDLADYFCQYNSYPLTFGAGTMDL 107
 RESULT 8
 KVIQ_HUMAN
 ID KVIQ_HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=68362076; PubMed=55951110;
 RA Hilschmann N.;
 RT Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.).*;
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RP REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,
 RL New York (1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01874; KIHURY.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;
 Query Match 63.6%; Score 362; DB 1; Length 108;
 Best Local Similarity 61.7%; Pred. No. 1.2e-32;
 Matches 66; Conservative 19; Mismatches 22; Indels 0; Gaps 0;
 QY 1 DIVVTQSHKFMSTVSGDRVSIICKASQDVGTAVDVTQKPGSPKLLIYWASTR 60
 DB 1 DIVVTQSPDSLAVSLGERATINCKSSQVLYSSNKNLAWYQKPGQPKLLIYWASTR 60

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Db 1 DIOMTQSPSSLSASVGDRTVITCQASQDISIFLNWYQORPGKAPKLLIYDASKLEAGVPS 60
QY 61 RFTGSGSGTDFLTITINVOSEDLDYFCQYNSYPLTFGAGTMDLKL 107
    ||:||||| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 61 RESGSGTDFLTITISLQPEDIAIYCCQDFNLPLTFGGTKVDFK 107
    ||:||||| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|

RESULT 9
KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlentz H.D.,
  Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
  single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
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CC -----
DR EMBL; 200022; CAAT7317.1; -
DR PIR; A01904; K4HUJ1.
DR HSSP; P80362; LWTLL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 5FB3953066744AF4 CRC64;

Query Match 63.4%; Score 360.5; DB 1; Length 133;
Best Local Similarity 61.1%; Pred. No. 2.3e-32;
Matches 69; Conservative 20; Mismatches 17; Indels 7; Gaps 2;

QY 1 DIYMTQSHKFMSTSVGDRYSIICKASQDV-----GTAVDWYQORPGQSPKLLIYWASTR 54
    ||||| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 21 DIYMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKYLAWYQORPGQSPKLLIYWASTR 80
    ||||| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|

QY 55 HTGVPRFTGSGSGTDFLTITINVOSEDLDYFCQYNSYPLTFGAGTMDLKL 107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 ESGVPRFTGSGSGTDFLTITISLQAEADVAVIYCCQYDTIP-TFGGTRKVEIK 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
KVIV_HUMAN STANDARD; PRT; 108 AA.
ID KVIV_HUMAN

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AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUEN.
DR HSSP; P80362; LWTLL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 62.9%; Score 358; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 3.4e-32;
Matches 68; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 1 DIYMTQSHKFMSTSVGDRYSIICKASQDVGTAVDWYQORPGQSPKLLIYWASTRHTGVDP 60
    ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSVYNYVAMVQORPGKAPKSLIYDASTLQSGVPS 60
    ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|

QY 61 RFTGSGSGTDFLTITINVOSEDLDYFCQYNSYPLTFGAGTMDLKL 107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NFTGSGSGTDFLTITISLQPEDPATYICQYNSYPTFGGTRKVIK 107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
KVIL_HUMAN STANDARD; PRT; 108 AA.
AC P01604;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Kue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eulitz M., Kley H.-P., Zeitler H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
  sequence of the variable part of a human I-chain of the kappa-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -|- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01870; KIHUKD.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

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DE Ig kappa chain V-V region HP RL6.7.
OC Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVMASR.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Antiarsonate antibody.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 61.9%; Score 352; DB 1; Length 108;
Best Local Similarity 59.8%; Pred. No. 1.5e-31;
Matches 64; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

Oy 1 DIVMTQSHKFMSTVGDRVSIICRASQDVGTAVDWYQOKPGQSPKLLIYNASTRTHTGVDP 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 DIOMTQTSSLASGLDRVTISCRASQDISNLYNMYQOKPDGTVKLLIYVTSRLHSGVPS 60

Oy 61 RFTGSGSGTDPTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 RFSGSGSGTDPTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107

RESULT 15
KV3H_HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curo J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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CC -----
CC EMBL; M12740; AAA58992.1; -.
DR PIR: A01898; K3HUCI.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JKL SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 61.4%; Score 349.5; DB 1; Length 129;
Best Local Similarity 61.1%; Pred. No. 3.5e-31;
Matches 66; Conservative 19; Mismatches 22; Indels 1; Gaps 1;

Oy 1 DIVMTQSHKFMSTVGDRVSIICRASQDVGTAVDWYQOKPGQSPKLLIYNASTRTHTGVDP 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQPPRLIYGASTATGIPA 80

Oy 61 RFTGSGSGTDPTLTITNVQSEDLADYFCQYNSY-PLTFGAGTMDLKL 107
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
81 RFSGSGSGTEFTLTISRLQSEDFAVYVCOYNNPPWTFGGGTRVEIK 128

Search completed: July 21, 2003, 13:31:53
Job time : 12.5315 secs
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Result No.	Query #			DB	ID	Description
	Score	Match	Length			
1	451	79.3	108	11	Q8V1J0	mus musculus
2	370	65.0	99	11	Q9JL74	mus musculus
3	361	63.4	108	4	Q9UL79	homo sapien
4	360	63.3	108	4	Q9UL79	homo sapien
5	359	63.1	108	4	Q9UL83	homo sapien
6	353.5	62.1	109	4	Q9UL85	homo sapien
7	349.5	61.4	109	4	Q9UL78	homo sapien
8	344	60.5	107	11	Q9ER29	mus musculus
9	343.5	60.4	107	4	Q96SA9	homo sapien
10	342	60.1	234	11	Q8R062	mus musculus
11	341	59.9	234	11	Q91WF8	mus musculus
12	340	59.8	108	4	Q9UL77	homo sapien
13	340	59.8	116	4	Q96PF6	homo sapien
14	338.5	59.5	107	4	Q9UL81	homo sapien
15	335	58.9	233	11	Q91WS9	mus musculus
16	324.5	57.0	238	11	Q99M37	mus musculus


```

DE DE Myosin-reactive immunoglobulin light chain variable region
DE OS (Fragment).
DE OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 63.1%; Score 359; DB 4; Length 108;
Best Local Similarity 60.7%; Pred. No. 4.7e-32;
Matches 65; Conservative 21; Mismatches 21; Indels 0; Gaps 0;

Qy 1 DIVTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60
Db 1 EIVTQSPATLSVSPGERATLSQVSSNLAWSYQKPGAPRLIYGASTRATGIPA 60

Qy 61 RFTGSGSGTDTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107
Db 1 RFTGSGSGTDTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107

Qy 61 RFTGSGSGTDTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107

RESULT 6
Q9UL85
ID Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56265.1; -.
DR HSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 62.1%; Score 353.5; DB 4; Length 109;
Best Local Similarity 62.0%; Pred. No. 1.9e-31;
Matches 67; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

Qy 1 DIVTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVPD 60

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Db 1 EIVTQSPATLSVSPGERATLSQVSSNLAWSYQKPGAPRLIYGASTRATGIPA 60
Qy 61 RFTGSGSGTDTLTITNVQSEDLADYFCQYNSY-PLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107

RESULT 7
Q9UL78
ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 61.4%; Score 349.5; DB 4; Length 109;
Best Local Similarity 60.2%; Pred. No. 5.3e-31;
Matches 65; Conservative 22; Mismatches 20; Indels 1; Gaps 1;

Qy 1 DIVTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQKPGQSPKLLIYWASTRHTGVP 59
Db 1 EIVTQSPGTLSPGERATLSQVSSNLAWSYQKPGQAPRLIYGASTRATGIP 60

Qy 60 RFTGSGSGTDTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107
Db 61 RFTGSGSGTDTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDLKL 107

RESULT 8
Q9ER29
ID Q9ER29 PRELIMINARY; PRT; 107 AA.
AC Q9ER29;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;

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Construction and sequencing of the single-chain antibody gene of a human TNF- α specific monoclonal antibody.;
Ti 4 Chun 1 Ta Hsueh Hsueh Pao 19:373-376(1998).

SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF262753; AAG23804.1; -;
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 60.5%; Score 344; DB 11; Length 107;
Best Local Similarity 61.7%; Pred. No. 2.1e-30;
Matches 66; Conservative 18; Mismatches 17; Indels 6; Gaps 1;

QY 4 MTQSHKFMSTVGDVRSIIICKASQDVGTGTA-----VDWYQKPGSPKLLIYWASTRTWG 57
Db 1 MTQSPSSLSASVGDVRSIIICKASQDVGTGTA-----VDWYQKPGSPKLLIYWASTRTWG 57
QY 58 VPDRTGSGGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDL 104
Db 61 VPDRTGSGGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDL 104

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ID Q96SA9
AC Q96SA9
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4B43E9C5B577F16 CRC64;

Query Match 60.4%; Score 343.5; DB 4; Length 107;
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Db 61 RFTGSGGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDL 106

RESULT 10

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AC Q96SA9
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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
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DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4B43E9C5B577F16 CRC64;

Q8R062

ID Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC027418; AAH27418.1; -;
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4E808C81426A8B1 CRC64;

Query Match 60.1%; Score 342; DB 11; Length 234;
Best Local Similarity 56.1%; Pred. No. 9.3e-30;
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QY 1 DIVMTQSHKFMSTVGDVRSIIICKASQDVGTGTA-----VDWYQKPGSPKLLIYWASTRTWG 60
Db 21 DIVMTQSHKFMSTVGDVRSIIICKASQDVGTGTA-----VDWYQKPGSPKLLIYWASTRTWG 60
QY 61 RFTGSGGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDL 107
Db 81 RFTGSGGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDL 127

RESULT 11

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AC Q91WF8
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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Mus.
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RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
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DR Pfam; PF00047; Ig; 2.
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KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6B7812D2 CRC64;

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ID Q91WF8
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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC015292; AAH15292.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6B7812D2 CRC64;

RT

human TNF- α specific monoclonal antibody.*;
Ti 4 Chun 1 Ta Hsueh Hsueh Pao 19:373-376(1998).

SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF262753; AAG23804.1; -;
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 60.5%; Score 344; DB 11; Length 107;
Best Local Similarity 61.7%; Pred. No. 2.1e-30;
Matches 66; Conservative 18; Mismatches 17; Indels 6; Gaps 1;

QY 4 MTQSHKFMSTVGDVRSIIICKASQDVGTGTA-----VDWYQKPGSPKLLIYWASTRTWG 57
Db 1 MTQSPSSLSASVGDVRSIIICKASQDVGTGTA-----VDWYQKPGSPKLLIYWASTRTWG 57
QY 58 VPDRTGSGGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDL 104
Db 61 VPDRTGSGGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDL 104

RESULT 9

Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4B43E9C5B577F16 CRC64;

Query Match 60.4%; Score 343.5; DB 4; Length 107;
Best Local Similarity 62.0%; Pred. No. 2.4e-30;
Matches 67; Conservative 19; Mismatches 19; Indels 3; Gaps 2;

QY 1 DIVMTQSHKFMSTVGDVRSIIICKASQDVGTGTA-----VDWYQKPGSPKLLIYWASTRTWG 60
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Db 61 RFTGSGGTDFTLTITNVQSEDLADYFCQYNSYPLTFGAGTMDL 106

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ID Q96SA9
AC Q96SA9
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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
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DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
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DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4B43E9C5B577F16 CRC64;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:32:31 ; Search time 34.7072 Seconds
(without alignments)
393.503 Million cell updates/sec

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Perfect score: 619
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	619	100.0	115	12	US-09-929-546-8	Sequence 8, Appli
3	619	100.0	130	12	US-09-929-665-4	Sequence 4, Appli
4	619	100.0	130	12	US-09-929-546-4	Sequence 4, Appli
5	496	80.1	117	11	US-09-956-206A-76	Sequence 76, Appl
6	496	80.1	136	11	US-09-956-206A-47	Sequence 47, Appl
7	493.5	79.7	232	10	US-09-754-998-2	Sequence 2, Appli
8	492	79.5	118	12	US-09-802-083-5	Sequence 5, Appli
9	492	79.5	118	15	US-10-165-732A-5	Sequence 5, Appli
10	491	79.3	125	12	US-09-929-665-20	Sequence 20, Appl
11	491	79.3	125	12	US-09-929-546-20	Sequence 20, Appl
12	486.5	78.6	672	12	US-09-900-766-1	Sequence 1, Appli
13	485	78.4	119	10	US-09-811-123-1	Sequence 1, Appli
14	485	78.4	119	15	US-10-268-501-2	Sequence 2, Appli
15	484	78.2	132	11	US-09-982-107-14	Sequence 14, Appl
16	484	78.2	669	11	US-09-807-721-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

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; Sequence 8, Application US/09929665
; Publication No. US20030003101A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-8

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Sequence 13, Appli
Sequence 18, Appli
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Sequence 78, Appli
Sequence 63, Appli
Sequence 30, Appli
Sequence 10, Appli
Sequence 7, Appli
Sequence 14, Appli
Sequence 10, Appli

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US-09-929-546-4			
; Sequence 4, Application US/09929546			
; Publication No. US20030031673A1			
; GENERAL INFORMATION:			
; APPLICANT: Bander, Neil H.			
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER			
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/028			
; CURRENT APPLICATION NUMBER: US/09/929,546			
; CURRENT FILING DATE: 2001-08-13			
; PRIOR APPLICATION NUMBER: 09/357,708			
; PRIOR FILING DATE: 1999-07-20			
; PRIOR APPLICATION NUMBER: US 08/838,682			
; PRIOR FILING DATE: 1997-04-09			
; PRIOR APPLICATION NUMBER: US 60/016,976			
; PRIOR FILING DATE: 1996-05-06			
; PRIOR APPLICATION NUMBER: US 60/022,125			
; PRIOR FILING DATE: 1996-07-18			
; NUMBER OF SEQ ID NOS: 21			
; SOFTWARE: PatentIn version 3.0			
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; TYPE: PRT			
; ORGANISM: Mus sp.			
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Query Match 100.0%; Score 619; DB 12; Length 130;			
Best Local Similarity 100.0%; Pred. No. 5.9e-48;			
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; Sequence 76, Application US/09956206A			
; Patent No. US20020164339A1			
; GENERAL INFORMATION:			
; APPLICANT: DO COUTO, FERNANDO J.R.			
; CERIANI, ROBERTO L.			
; PETERSON, JERRY A.			
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE			
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND			
; METHODS OF HUMANIZING ANTIBODY PEPTIDES			
; NUMBER OF SEQUENCES: 81			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: MORRISON & FOERSTER			
; STREET: 755 page Mill Road			
; CITY: Palo Alto			
; STATE: CA			
; COUNTRY: USA			
; ZIP: 94304-1018			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/956,206A			
; FILING DATE: 19-Apr-2002			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			

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; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-956-206A-76
Query Match 80.1%; Score 496; DB 11; Length 117;
Best Local Similarity 78.6%; Pred. No. 4.5e-37;
Matches 92; Conservative 11; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVLOQSGPELVKPGTSVRISKTSQYTFETIHWKSHGSKSLWIGNINPNNGGTTY 60
DB 1 EVLOQSGPELVKPGASKISCEASGYSTGYTMHWKSHGSHGNLEWIGLINPYNGGTVY 60
QY 61 NKFEDKATLTVDKSSSTAYMELSLTSDSAVYYCAAGWNE--DYWGOGTTLTVSS 115
DB 61 NKFQDKATLTVDKSSGTAYMELLSLTSSESAVYFCARRRWTMDYWGOGTSVTSS 117

RESULT 6
US-09-956-206A-47
; Sequence 47, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995

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; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WITT, ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-956-206A-47
Query Match 80.1%; Score 496; DB 11; Length 136;
Best Local Similarity 78.6%; Pred. No. 5.2e-37;
Matches 92; Conservative 11; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVLOQSGPELVKPGTSVRISKTSQYTFETIHWKSHGSKSLWIGNINPNNGGTTY 60
DB 20 EVLOQSGPELVKPGASKISCEASGYSTGYTMHWKSHGSHGNLEWIGLINPYNGGTVY 79
QY 61 NKFEDKATLTVDKSSSTAYMELSLTSDSAVYYCAAGWNE--DYWGOGTTLTVSS 115
DB 80 NKFQDKATLTVDKSSGTAYMELLSLTSSESAVYFCARRRWTMDYWGOGTSVTSS 136

RESULT 7
US-09-754-998-2
; Sequence 2, Application US/09754998
; Patent No. US20020002271A1
; GENERAL INFORMATION:
; APPLICANT: Rinderknecht, Ernst H.
; Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY PURIFICATION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,998
; FILING DATE: 04-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,757
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 941
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-754-938-2

Query Match
Best Local Similarity 79.7%; Score 493.5; DB 10; Length 232;
Matches 94; Conservative 10; Mismatches 11; Indels 9; Gaps 2;

QY 1 EVLQOQSGPELVKPGTSTVRISCKTSGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGTTY 60
DB 1 EVLQOQSGPELVKPGASVKIKCKTSGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGSSH 60
QY 61 NOKFEDKATLTVDKSSSTAYMELSLTSEDSAVYYCAA--AGWN-----FDYWGQGTTL 111
DB 61 NQRFMDKATLAVDKSTSTAYMELSLTSEDSGIYYCARWRLNYGFVRYFDVMGAGTTV 120
QY 112 TVSS 115
DB 121 TVSS 124

RESULT 8
US-09-802-083-5
; Sequence 5, Application US/09802083
; Publication No. US20030119075A1
; GENERAL INFORMATION:
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Presta, David G.
; TITLE OF INVENTION: Anti-Tissue Factor Antibodies with Enhanced
; TITLE OF INVENTION: Anticoagulant Potency
; FILE REFERENCE: PI/3681
; CURRENT APPLICATION NUMBER: US/09/802,083
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 5
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-802-083-5

Query Match
Best Local Similarity 79.5%; Score 492; DB 12; Length 118;
Matches 93; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVLQOQSGPELVKPGTSTVRISCKTSGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGTTY 60
DB 1 EVLQOQSGPELVKPGASVKIKCKASGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGNTIY 60
QY 61 NOKFEDKATLTVDKSSSTAYMELSLTSEDSAVYYCAA--GWNFDYWGQGTTLTVSS 115
DB 61 NQKFKGKATLTVDKSSSTAYLLESLTSEDYAVFCARDHDYDFDFWQGGTTLTVSS 117

RESULT 9
US-10-165-732A-5
; Sequence 5, Application US/10165732A
; Publication No. US20030124117A1
; GENERAL INFORMATION:
; APPLICANT: Refino, Canio J.
; APPLICANT: Bunting, Stuart
; APPLICANT: Kirchhofer, Daniel
; TITLE OF INVENTION: COMBINATIONS OF ANTI-TISSUE FACTOR ANTIBODIES AND ANTICOAGULANT A
; TITLE OF INVENTION: ANTIPATELET AGENTS
; FILE REFERENCE: 11669.110US11
; CURRENT APPLICATION NUMBER: US/10/165,732A
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/802,083
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-165-732A-5

Query Match
Best Local Similarity 79.5%; Score 492; DB 15; Length 118;
Matches 93; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVLQOQSGPELVKPGTSTVRISCKTSGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGTTY 60
DB 1 EVLQOQSGPELVKPGASVKIKCKASGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGNTIY 60
QY 61 NOKFEDKATLTVDKSSSTAYMELSLTSEDSAVYYCAA--GWNFDYWGQGTTLTVSS 115
DB 61 NQKFKGKATLTVDKSSSTAYLLESLTSEDYAVFCARDHDYDFDFWQGGTTLTVSS 117

RESULT 10
US-09-929-665-20
; Sequence 20, Application US/09929665
; Publication No. US20030003101A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: B2L 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-20

Query Match
Best Local Similarity 79.3%; Score 491; DB 12; Length 125;
Matches 96; Conservative 10; Mismatches 9; Indels 10; Gaps 2;

QY 1 EVLQOQSGPELVKPGTSTVRISCKTSGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGTT 59
DB 1 EVLQOQSGPELVKPGASVKIKCKASGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGTS 60
QY 60 YNKFEDKATLTVDKSSSTAYMELSLTSEDSAVYYCAAG-----WNPFDYWGQGT 110
DB 61 YNKFEGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARGYSSSYMAYAFDYWGQGT 120
QY 111 LTSS 115
DB 121 TVSS 125

RESULT 11
US-09-929-546-20
; Sequence 20, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: B2L 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
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; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; SOFTWARE: PatentIn version 3.0
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 20
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-546-20

Query Match          79.3%; Score 491; DB 12; Length 125;
Best Local Similarity 76.8%; Pred. No. 1.3e-36;
Matches 96; Conservative 10; Mismatches 9; Indels 10; Gaps 2;

Qy 1 EVQLQSGPELVKPGTSVIRISCKTSGYTFTETI-HVVKQSHGKSLWIGINPNNGGTT 59
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLQSGPELVKPGASVKISCKASGYFTDYNNVNVKQSPGKSLWIGIDINFCNGGTS 60

Qy 60 YNQFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCAAG-----WNFDYWGOGTT 110
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 YNQFEDKATLTVDKSSSTAYMQLSLTSDSAVYYCARGYSSSYMAYVAFDYWGOGTT 120

Qy 111 LTVSS 115
Db 121 VTVSS 125

RESULT 12
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US;10104199
; CURRENT APPLICATION NUMBER: US/09/900.766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match          78.6%; Score 486.5; DB 12; Length 672;
Best Local Similarity 77.5%; Pred. No. 2e-35;
Matches 93; Conservative 9; Mismatches 13; Indels 5; Gaps 1;

Qy 1 EVQLQSGPELVKPGTSVIRISCKTSGYTFTETIHWVKQSHGKSLWIGINPNNGGTTY 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLQSGPELVKPGASVKISCKASGYFTCYMHWVKQSPGKLEWIGINPNNGVTLY 60

Qy 61 NQPFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCA-----AGWNFDYWGOGTTLVSS 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NQPFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCARSTMTITVYVMDYWGOGTSVTVSS 120

RESULT 13
US-09-811-123-1
```

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; Sequence 1, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Slikowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811.123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-1

Query Match          78.4%; Score 485; DB 10; Length 119;
Best Local Similarity 75.6%; Pred. No. 4.3e-36;
Matches 90; Conservative 14; Mismatches 11; Indels 4; Gaps 1;

Qy 1 EVQLQSGPELVKPGTSVIRISCKTSGYTFTETIHWVKQSHGKSLWIGINPNNGGTTY 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLQSGPELVKPGTSVKISCKASGFTFTDTMDVVKQSHGKSLWIGDVPNNGSGSIY 60

Qy 61 NQPFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCA-----AGWNFDYWGOGTTLVSS 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NQPFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCARNLGSPSYFDYWGOGTTLVSS 119

RESULT 14
US-10-268-501-2
; Sequence 2, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Slikowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P146782P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-268-501-2

Query Match          78.4%; Score 485; DB 15; Length 119;
Best Local Similarity 75.6%; Pred. No. 4.3e-36;
Matches 90; Conservative 14; Mismatches 11; Indels 4; Gaps 1;

Qy 1 EVQLQSGPELVKPGTSVIRISCKTSGYTFTETIHWVKQSHGKSLWIGINPNNGGTTY 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLQSGPELVKPGTSVKISCKASGFTFTDTMDVVKQSHGKSLWIGDVPNNGSGSIY 60

Qy 61 NQPFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCA-----AGWNFDYWGOGTTLVSS 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NQPFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCARNLGSPSYFDYWGOGTTLVSS 119

RESULT 15
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C37267
Ig heavy chain V region (Py69) - mouse
C.Species: Mus musculus (house mouse)
C.Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C.Accession: C37267
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A.Title: Heavy and light chain variable region sequences and antibody properties
A.Reference number: A38740; MUID:91177923; PMID:1706720
A.Accession: C37267
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F.19-102/Domain: immunoglobulin homology <IMM>

Query Match 85.4%; Score 528.5; DB 2; Length 128;
Best Local Similarity 81.3%; Pred. No. 1.4e-39;
Matches 100; Conservative 7; Mismatches 7; Indels 9; Gaps 1;

QY 2 VOLQSGPELVKPGTGSVRISCKTSGYTFTEYTHHWKSHGKSLWIGNINPNNGGTTYN 61
DB 6 VOLQSGPELVKPGASVKISCKTSGYTFTEYTHHWKSHGKSLWIGNINPNNGGTTYN 65
QY 62 QKFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCA-----AGNFDYWGQGTTLT 112
DB 66 QKFRGKATLTVDKSSSTAYMELRSLTSDSAVYYCARRGPGYNYTTSYFYDYWGQGTTLT 125
QY 113 VSS 115
DB 126 VSS 128

RESULT 3

A37267
Ig heavy chain V region (Py20) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: A37267
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A36740; MUID:91177923; PMID:1706720
A:Accession: A37267
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 512.5; DB 2; Length 128;
Best Local Similarity 79.0%; Pred. No. 3.5e-38;
Matches 98; Conservative 8; Mismatches 9; Indels 9; Gaps 1;
QY 1 EVOLQSGPELVKPGTGSVRISCKTSGYTFTEYTHHWKSHGKSLWIGNINPNNGGTTY 60
DB 5 EVOLQSGPELVKPGASVKISCKTSGYTFTEYTHHWKSHGKSLWIGNINPNNGGTRD 64
QY 61 NQKFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCAA-----GNFDYWGQGTTL 111
DB 65 NQFRGKATLTVDKSSSTAYMELRSLTSDSAVYYCARRGPGYNYTTSYFYDYWGQGTTL 124
QY 112 TVSS 115
DB 125 TVSS 128

RESULT 4

F37266
Ig heavy chain V region (Py2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: F37266
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A36740; MUID:91177923; PMID:1706720
A:Accession: F37266
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-121 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-100/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 512; DB 2; Length 121;
Best Local Similarity 85.6%; Pred. No. 3.7e-38;

Matches 101; Conservative 3; Mismatches 8; Indels 6; Gaps 2;
QY 2 VOLQSGPELVKPGTGSVRISCKTSGYTFTEYTHHWKSHGKSLWIGNINPNNGGTTYN 61
DB 6 VOLQSGPELVKPGASVKISCKTSGYTFTEYTHHWKSHGKSLWIGNINPNNGGTT--N 63
QY 62 QKFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCAAG---WNFDYWGQGTTLTVSS 115
DB 64 QKFRGKATLTVDKSSSTAYMELRSLTSDSAVYYCARRGDNLYYFDYWGQGTTLTVSS 121

RESULT 5

S55535
Ig heavy chain V region pe23 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C:Accession: S55535
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies u-
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <BOE>
A:Cross-references: EMBL:X82592; NID:g854310; PIDN:CAA57928.1; PID:g854311
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 510.5; DB 2; Length 113;
Best Local Similarity 85.1%; Pred. No. 4.6e-38;
Matches 97; Conservative 8; Mismatches 8; Indels 1; Gaps 1;
QY 2 VOLQSGPELVKPGTGSVRISCKTSGYTFTEYTHHWKSHGKSLWIGNINPNNGGTTYN 61
DB 1 VOLQSGPELVKPGASVKISCKTSGYTFTEYTHHWKSHGKSLWIGNINPNNGRTSYN 60
QY 62 QKFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCAAGNFDYWGQGTTLTVSS 115
DB 61 QKFDKAPLTVDKASSTAYMEVRLTSDSAVYFCARG--DVAYWGQGTTVTVSS 113

RESULT 6

MMS38
Ig heavy chain V region (AC38 205.12) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 30-May-1997
C:Accession: A02040
R:Dildrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.
EMBO J. 3, 517-523, 1984
A:Title: A V region determinant (idiotope) expressed at high frequency in B lymphocyte
A:Reference number: A91000; MUID:84182519; PMID:6201362
A:Accession: A02040
A:Molecule type: protein
A:Residues: 1-118 <DIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-98/Region: V segment
F:15-98/Domain: immunoglobulin homology <IMM>
F:99-104/Region: D segment
F:105-118/Region: J segment
F:22-96/Disulfide bonds: #status predicted

Query Match 82.1%; Score 508.5; DB 1; Length 118;
Best Local Similarity 81.4%; Pred. No. 7.3e-38;
Matches 96; Conservative 9; Mismatches 10; Indels 3; Gaps 1;
QY 1 EVOLQSGPELVKPGTGSVRISCKTSGYTFTEYTHHWKSHGKSLWIGNINPNNGGTTY 60
DB 1 EVOLQSGPELVKPGASVKISCKASGYTFTDYIMNWKSHGKSLWIGDINPNNGGTSY 60

Search completed: July 21, 2003, 13:33:21
Job time : 26.3829 secs

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehy M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin v region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 81.6%; Score 505; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 2.2e-42;
Matches 95; Conservative 9; Mismatches 11; Indels 2; Gaps 1;

QY 1 EVQLQSGPELVKPGTSTSRISCKTSYTFETTHHWKSHGKSLSEWIGNINPNNGGTTY 60
DB 1 EVQLQSGPELVKPGASVKMSKASGYTFDYMKNWVKSHGKSLSEWIGDINPNNGGTSY 60
QY 61 NQKFKGKATLTVDKSSSTAYMELRSLTSDSVAVYCAA--GNFDYWGOGTTLTVSS 115
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSVAVYCARDYDFWVWAGTTVTVSS 117

RESULT 3
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain v region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain v-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin v region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 81.6%; Score 505; DB 1; Length 117;

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Best Local Similarity 81.2%; Pred. No. 2.2e-42;
Matches 95; Conservative 9; Mismatches 11; Indels 2; Gaps 1;

QY 1 EVQLQSGPELVKPGTSTSRISCKTSYTFETTHHWKSHGKSLSEWIGNINPNNGGTTY 60
DB 1 EVQLQSGPELVKPGASVKMSKASGYTFDYMKNWVKSHGKSLSEWIGDINPNNGGTSY 60
QY 61 NQKFKGKATLTVDKSSSTAYMELRSLTSDSVAVYCAA--GNFDYWGOGTTLTVSS 115
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSVAVYCARDYDFWVWAGTTVTVSS 117

RESULT 4
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain v region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
DR EMBL; J00529; AAA38170.1; -.
DR PIR; A02034; MHMS18.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match 73.9%; Score 457.5; DB 1; Length 139;
Best Local Similarity 72.5%; Pred. No. 1.1e-37;
Matches 87; Conservative 10; Mismatches 18; Indels 5; Gaps 1;

QY 1 EVQLQSGPELVKPGTSTSRISCKTSYTFETTHHWKSHGKSLSEWIGNINPNNGGTTY 60
DB 20 QVQLQQPGLVLPKPGASVKLSCKASGYTFTSYMMHWVKRPGRLGLEWIGRIDPNSGGTTY 79

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OY 61 NQFEDKATLVKSSSTAYMELRLTSEDSAVYYCA-----AGWNFDYWGQGTTLTVSS 115
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL; J00539; AAA38172.1; -.
CC PIR; A02038; G2MS43.
CC HSSP; P01810; 2FBU.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 122 D SEGMENT.
CC DOMAIN 123 137 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON_TER 137 137
CC SEQUENCE 137 AA; ADD5881BF44B8EC9 CRC64;

Query Match 73.38; Score 453.5; DB 1; Length 137;
Best Local Similarity 72.08; Pred. No. 2.6e-37;
Matches 85; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

OY 1 EVOLQSGPELVKPTSVRISCKTSGYTFEYTHVWKQSHGKSLWIGNINPNNGGTTY 60
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Broder P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
```

RT idotype response of the strain A mouse.*;
 RL Eur. J. Immunol. 12:1023-1032(1982).
 CC -I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
 CC SEGMENT, JH2.
 DR PIR; A02028; HVMSG7.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 KW Immunoglobulin v region; Antiarsonate antibody; Hybridoma.
 FT NON_TER 120
 SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
 Query Match 71.7%; Score 444; DB 1; Length 120;
 Best Local Similarity 71.7%; Pred. No. 1.9e-36;
 Matches 86; Conservative 11; Mismatches 17; Indels 6; Gaps 1;
 QY 2 VOLQSGPELVKPGTSVRISCKTSGYTFETTHVVKOSHGKSLWIGNINPNNGGTTYN 61
 DB 1 VOLQSGAELVRAGSSVVKMSCKASGYTFSTGGINVVKRPGQGLEWIGTINPGNGYTYIN 60
 QY 62 QKFEDKATLTVDKSSSTAYMELRLSTSDSAVYYCA-----AGWNFDYWGQGTTLTVSS 115
 DB 61 EKFKCKTTLTVDKSSSTAYMQLRLSTSDSAVYFCARSHYVGGSYFDYWGQGTTLTVSS 120
 RESULT 8
 HV02_MOUSE
 ID HV02_MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Ig heavy chain v region 93G7 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A/J;
 RA MEDLINE=82152818; PubMed=6801765;
 RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
 RA Capra J.D.;
 RT "Somatic mutation in genes for the variable portion of the
 RT Immunoglobulin heavy chain.";
 RL Science 216:309-311(1982).
 CC -----
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 CC -----
 DR EMBL; J00493; AAA38128.1;
 DR PIR; A02028; HVMSG7.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 KW Immunoglobulin v region; Antiarsonate antibody; Hybridoma; Signal.
 FT SIGNAL 1
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
 Query Match 71.2%; Score 441; DB 1; Length 140;
 Best Local Similarity 71.7%; Pred. No. 1.9e-36;
 Matches 86; Conservative 11; Mismatches 17; Indels 6; Gaps 1;
 QY 2 VOLQSGPELVKPGTSVRISCKTSGYTFETTHVVKOSHGKSLWIGNINPNNGGTTYN 61
 DB 1 VOLQSGAELVRAGSSVVKMSCKASGYTFSTGGINVVKRPGQGLEWIGTINPGNGYTYIN 60
 QY 62 QKFEDKATLTVDKSSSTAYMELRLSTSDSAVYYCA-----AGWNFDYWGQGTTLTVSS 115
 DB 61 EKFKCKTTLTVDKSSSTAYMQLRLSTSDSAVYFCARSHYVGGSYFDYWGQGTTLTVSS 120
 RESULT 9
 HV14_MOUSE
 ID HV14_MOUSE STANDARD; PRT; 117 AA.
 AC P01758;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Ig heavy chain v region 108A precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=81245215; PubMed=6789211;
 RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
 RT "Diversity of germ-line immunoglobulin VH genes.";
 RL Nature 292:426-430(1981).
 CC -----
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 CC -----
 DR EMBL; J00488; AAA38519.1;
 DR PIR; A02041; HVMS8A.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 KW Immunoglobulin v region; Signal.
 FT SIGNAL 1
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;
 Query Match 70.8%; Score 438; DB 1; Length 117;
 Best Local Similarity 85.6%; Pred. No. 6.9e-36;
 Matches 83; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 EVQLOQSGPELVKPGTSVRISCKTSGYTFETTHVVKOSHGKSLWIGNINPNNGGTTTY 60
 DB 20 EVQLOQSGPELVKPGASVKISKASGYTFDTNMHWVKOSHGKSLWIGTYIPYNGGTGY 79
 QY 61 NOKFEDKATLTVDKSSSTAYMELRLSTSDSAVYYCA 97
 DB 80 NOKFESKATLTVDNSSSTAYMELSLSTSDSAVYYCA 116
 RESULT 10
 HV50_MOUSE
 ID HV50_MOUSE STANDARD; PRT; 120 AA.
 AC P06329;
 Query Match 71.2%; Score 441; DB 1; Length 140;
 Best Local Similarity 71.7%; Pred. No. 1.9e-36;
 Matches 86; Conservative 11; Mismatches 17; Indels 6; Gaps 1;
 QY 2 VOLQSGPELVKPGTSVRISCKTSGYTFETTHVVKOSHGKSLWIGNINPNNGGTTYN 61
 DB 1 VOLQSGAELVRAGSSVVKMSCKASGYTFSTGGINVVKRPGQGLEWIGTINPGNGYTYIN 60
 QY 62 QKFEDKATLTVDKSSSTAYMELRLSTSDSAVYYCA-----AGWNFDYWGQGTTLTVSS 115
 DB 61 EKFKCKTTLTVDKSSSTAYMQLRLSTSDSAVYFCARSHYVGGSYFDYWGQGTTLTVSS 120

Best Local Similarity 70.2%; Pred. No. 4.4e-36;
 Matches 85; Conservative 12; Mismatches 18; Indels 6; Gaps 1;
 QY 1 EVQLOQSGPELVKPGTSVRISCKTSGYTFETTHVVKOSHGKSLWIGNINPNNGGTTTY 60
 DB 20 EVQLOQSGAELVRAGSSVVKMSCKASGYTFSTGGINVVKRPGQGLEWIGTYIPYNGGTGY 79
 QY 61 NOKFEDKATLTVDKSSSTAYMELRLSTSDSAVYYCA-----AGWNFDYWGQGTTLTVSS 114
 DB 80 NEKFKCKTTLTVDKSSSTAYMQLRLSTSDSAVYFCARSHYVGGSYFDYWGQGTTLTVSS 139
 QY 115 S 115
 DB 140 S 140
 RESULT 9
 HV14_MOUSE
 ID HV14_MOUSE STANDARD; PRT; 117 AA.
 AC P01758;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Ig heavy chain v region 108A precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=81245215; PubMed=6789211;
 RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
 RT "Diversity of germ-line immunoglobulin VH genes.";
 RL Nature 292:426-430(1981).
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 CC -----
 DR EMBL; J00488; AAA38519.1;
 DR PIR; A02041; HVMS8A.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 KW Immunoglobulin v region; Signal.
 FT SIGNAL 1
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;
 Query Match 70.8%; Score 438; DB 1; Length 117;
 Best Local Similarity 85.6%; Pred. No. 6.9e-36;
 Matches 83; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 EVQLOQSGPELVKPGTSVRISCKTSGYTFETTHVVKOSHGKSLWIGNINPNNGGTTTY 60
 DB 20 EVQLOQSGPELVKPGASVKISKASGYTFDTNMHWVKOSHGKSLWIGTYIPYNGGTGY 79
 QY 61 NOKFEDKATLTVDKSSSTAYMELRLSTSDSAVYYCA 97
 DB 80 NOKFESKATLTVDNSSSTAYMELSLSTSDSAVYYCA 116
 RESULT 10
 HV50_MOUSE
 ID HV50_MOUSE STANDARD; PRT; 120 AA.
 AC P06329;


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DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 64.1%; Score 397; DB 1; Length 117;
Best Local Similarity 76.8%; Pred. No. 6.6e-32;
Matches 73; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 2 VOLQSGPELVKPGTSVRISCKTSGYTFEYTIHWVKQSHGKSLIEWIGNINPNNGGTTYN 61
Db 21 VOLQPGAEVLKPGASVKLSCKASGYFTSYMMHWKQRPGRGLEWIGNIDPNSGGTKYN 80
Qy 62 OKPEDKATLTVDKSSSTAYWELRSLTSEDSAVYYC 96
Db 81 EKPKSKATLTVDKPSPSTAYNQLSLSLTSEDSAVYYC 115

Search completed: July 21, 2003, 13:31:53
Job time : 14.4685 secs

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OM protein - protein search, using sw model

Run on: July 21, 2003, 13:29:50 ; Search time 50.7658 Seconds
(without alignments)
466.760 Million cell updates/sec

Title: US-09-929-546-8

Perfect score: 619

Sequence: 1 EVQLQSGPELVKPGTSTRI.....CAAGWFDYWGQGTTLTVSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	513	82.9	117	11	Q9QXF0 mus musculu
2	500	80.8	117	11	Q9QXE9 mus musculu
3	487	78.7	140	11	Q924P8 mus musculu
4	473.5	76.5	488	11	Q91WR1 mus musculu
5	473	76.4	142	11	Q924Q1 mus musculu
6	464	75.0	120	11	Q920E8 mus musculu
7	461	74.5	146	11	Q924R8 mus musculu
8	460	74.3	123	11	Q8VJ1 mus musculu
9	459.5	74.2	145	11	Q924R3 mus musculu
10	458.5	74.1	137	11	Q924R6 mus musculu
11	458.5	74.1	278	11	Q921K1 mus musculu
12	458.5	74.1	481	11	Q8VCV5 mus musculu
13	457.5	73.9	145	11	Q924Q7 mus musculu
14	454	73.3	140	11	Q924R2 mus musculu
15	453	73.2	144	11	Q924P5 mus musculu
16	450.5	72.8	143	11	Q924R0 mus musculu

17	450	72.7	146	11	Q924Q8 mus musculu
18	448.5	72.5	145	11	Q924R4 mus musculu
19	448.5	72.5	145	11	Q924R1 mus musculu
20	448.5	72.5	145	11	Q924Q9 mus musculu
21	448.5	72.5	145	11	Q924Q6 mus musculu
22	448	72.4	146	11	Q924Q3 mus musculu
23	446.5	72.1	143	11	Q924R7 mus musculu
24	446.5	72.1	143	11	Q924Q5 mus musculu
25	446.5	72.1	145	11	Q924P7 mus musculu
26	446	72.1	141	11	Q91WT1 mus musculu
27	444.5	71.8	141	11	Q924Q4 mus musculu
28	442.5	71.5	143	11	Q924Q0 mus musculu
29	442	71.4	170	11	Q925S2 mus musculu
30	441.5	71.3	143	11	Q91VA2 mus musculu
31	433.5	70.0	143	11	Q91V67 mus musculu
32	432.5	69.9	143	11	Q924P9 mus musculu
33	431.5	69.7	109	11	Q9JL75 mus musculu
34	430	69.5	473	11	Q9D8L4 mus musculu
35	429.5	69.4	143	11	Q924P6 mus musculu
36	429.5	69.4	473	11	Q9JL25 mus musculu
37	427.5	69.1	139	11	Q924R5 mus musculu
38	414.5	67.0	613	11	Q8VCX7 mus musculu
39	408.5	66.0	118	11	Q9Z1C4 mus musculu
40	408	65.9	489	11	Q8VCX4 mus musculu
41	407.5	65.8	114	11	Q9JL81 mus musculu
42	407	65.8	119	5	Q9GV22 schistosoma
43	404	65.3	142	11	Q924Q2 mus musculu
44	402.5	65.0	463	11	Q991C4 mus musculu
45	402	64.9	147	11	Q925S3 mus musculu

ALIGNMENTS

RESULT 1

Q9QXF0 PRELIMINARY; PRT; 117 AA.
ID AC Q9QXF0
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademackers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1;
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 82.9%; Score 513; DB 11; Length 117;
Best Local Similarity 82.9%; Pred. No. 1.9e-43;
Matches 97; Conservative 9; Mismatches 9; Indels 2; Gaps 1;

QY 1 EVQLQSGPELVKPGTSTRIKTSKSYTFTYTHWYKQSHGKSLKLEWGINPNNGGTTY 60
|||||
Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFDYIMKWKVQSHGKSLKLEWGINPNNGGTSY 60
|||||
QY 61 NQKFEKATLTVDKSSSTAYMELRLSTSEDSAVYYCA--AGWNPDYWGQGTTLTVSS 115
|||||
Db 61 NQKFEKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKDYFDYWGQGTTLTVSS 117
|||||

```
RESULT 2
Q9QXE9 PRELIMINARY; PRT; 117 AA.
ID Q9QXE9
AC Q9QXE9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1; -
DR HSP; P01810; 2FBJ
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 80.8%; Score 500; DB 11; Length 117;
Best Local Similarity 80.3%; Pred. No. 3.6e-42;
Matches 94; Conservative 11; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVLOQSGPELVKPGKTSVRISCKTSGYTFETIHWKQSHGKSLWIGNINPNNGGTTY 60
DB 1 EVLOQSGPELVKPGKSKASGYTFTDYMKWKQSHGKSLWIGDINPNNGGTSY 60
QY 61 NOKFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCAAG--WNFDYWGOGTTLTVSS 115
DB 61 NOKFEGKATLTVDKSSSTAYMQLNLTSDSAVYYTCARDRIYAMDYWGOGTSVTYSS 117

RESULT 3
Q924P8 PRELIMINARY; PRT; 140 AA.
ID Q924P8
AC Q924P8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RL "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069917; BAB63933.1; -
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1
FT 140
SQ SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;

Query Match 78.7%; Score 487; DB 11; Length 140;
Best Local Similarity 77.4%; Pred. No. 8.8e-41;
Matches 89; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLOQSGPELVKPGKTSVRISCKTSGYTFETIHWKQSHGKSLWIGNINPNNGGTTY 60
DB 1 EVLOQSGPELVKPGKSKASGYTFTDYMKWKQSHGKSLWIGDINPNNGGTSY 60

RESULT 4
Q91WR1 PRELIMINARY; PRT; 488 AA.
ID Q91WR1
AC Q91WR1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 53.0 kDa protein.
GN AI893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AAH13539.1; -
DR MGD; MGI:2144917; AI893585.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 76.5%; Score 473.5; DB 11; Length 488;
Best Local Similarity 71.8%; Pred. No. 8.9e-39;
Matches 89; Conservative 16; Mismatches 10; Indels 9; Gaps 2;

QY 1 EVLOQSGPELVKPGKTSVRISCKTSGYTFETIHWKQSHGKSLWIGNINPNNGGTTY 60
DB 20 EVLOQSGPELVKPGKSKASGYTFTDYMKWKQSHGKSLWIGDINPNNGGTSY 79
QY 61 NOKFEDKATLTVDKSSSTAYMELRSLTSDSAVYYCAAG---WNF-----DYWGOGTTL 111
DB 80 NOKFEGKATLTVDKSSSTAYMQLNLTSDSAVYYTCARGPVVYYSFYSDRGDYWGOGTTLV 139
QY 112 TVSS 115
DB 140 TVSA 143

RESULT 5
Q924Q1 PRELIMINARY; PRT; 142 AA.
ID Q924Q1
AC Q924Q1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069913; BAB63929.1; -
DR InterPro: IPR003006; Ig_MHC.
```


Db 61 SOKFKDKATLVKDSRTAYMQLNSLTSEDSAVYYCARDYTYTYDEGCFAYWGQGLTV 120

QY 113 VSS 115

Db 121 VSA 123

RESULT 9
Q924R3

ID Q924R3 PRELIMINARY; PRT: 145 AA.
AC Q924R3; 74.2%; Score 459.5; DB 11; Length 145;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067787; BAB63272.1;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
FT NON_TER 1 145
FT TER 145 145
SQ SEQUENCE 145 AA; 15996 MW; 35B1A36E4280BA81 CRC64;

Query Match 74.2%; Score 459.5; DB 11; Length 145;
Best Local Similarity 71.7%; Pred. No. 4.9e-38;
Matches 86; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

QY 1 EVOLQSGPELVKPGCTSVRIKCTSGYTFETTHWVKQSHGKSLEWIGNINPNNGGTTY 60

Db 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKQRRGGLWIGRIDPNSSGGTKY 60

QY 61 NOKFEDKATLVKDSRTAYMELRLSLTSEDSAVYYCAAG-----WNFDYWGQGLTLYSS 115

Db 61 NEKFKSKATLVKDSRTAYMQLNSLTSEDSAVYYCARGLYDGNVYFDWVGTTVTYSS 120

RESULT 10

ID Q924R6 PRELIMINARY; PRT: 137 AA.
AC Q924R6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067783; BAB63268.1;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
FT NON_TER 1 137
FT TER 137 137

SQ SEQUENCE 137 AA; 15171 MW; 5C38D966DC6A4124 CRC64;
Query Match 74.1%; Score 458.5; DB 11; Length 137;
Best Local Similarity 74.8%; Pred. No. 5.8e-38;
Matches 86; Conservative 11; Mismatches 15; Indels 3; Gaps 1;

QY 1 EVOLQSGPELVKPGCTSVRIKCTSGYTFETTHWVKQSHGKSLEWIGNINPNNGGTTY 60

Db 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKQRRGGLWIGRIDPNSSGGTKY 60

QY 61 NOKFEDKATLVKDSRTAYMELRLSLTSEDSAVYYCAAGWNPFDYWGQGLTLYSS 115

Db 61 NEKFKSKATLVKDSRTAYMQLNSLTSEDSAVYYCA---RMDYWGQGLTLYSS 112

RESULT 11

ID Q921K1 PRELIMINARY; PRT: 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Unknown (protein for MGC:18977).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1;
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 74.1%; Score 458.5; DB 11; Length 278;
Best Local Similarity 70.8%; Pred. No. 1.4e-37;
Matches 85; Conservative 12; Mismatches 18; Indels 5; Gaps 1;

QY 1 EVOLQSGPELVKPGCTSVRIKCTSGYTFETTHWVKQSHGKSLEWIGNINPNNGGTTY 60

Db 20 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKQRRGGLWIGRIDPNSSGGTKY 79

QY 61 NOKFEDKATLVKDSRTAYMELRLSLTSEDSAVYYCAAGWN-----FDYWGQGLTLYSS 115

Db 80 NEKFKSKATLVKDSRTAYMQLNSLTSEDSAVYYCTRGYGYDDVYFDWVGAGTTVTYSS 139

RESULT 12

ID Q8VCV5 PRELIMINARY; PRT: 481 AA.
AC Q8VCV5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018455; AAH18455.1;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; Ig; 3.

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DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match
Best Local Similarity 74.1%; Score 458.5; DB 11; Length 481;
Matches 84; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

Oy 1 EVOLQSQPELVKPGKTSVRISCKTSGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGTTY 60
Db 20 EIQLQQSGPELVKPGTSVKSKASGYTFIDYINHWKQSHGKSLSEWIGYIDPYNGSSY 79

Oy 61 NOKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAGWN---FDYWGQGTTLTVSS 115
Db 80 NOKFKRATLTVDKSSNTAFMYLNNLTSEDSAFYYCAREWYGAWFAGQGTTLTVSA 137

RESULT 13
O92407 PRELIMINARY; PRT; 145 AA.
AC -O92407:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 145
FT NON_TER 145
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match
Best Local Similarity 73.9%; Score 457.5; DB 11; Length 145;
Matches 87; Conservative 10; Mismatches 18; Indels 5; Gaps 1;

Oy 1 EVOLQSQPELVKPGKTSVRISCKTSGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGTTY 60
Db 1 QVQLQQPQGAELVKGASVKLSCKASGYTFTSYWMHWKQRPGRGLEWIGRIDPNSSGGTKY 60

Oy 61 NOKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCA-----AGNFDYWGQGTTLTVSS 115
Db 61 NEKFKRATLTVDKPSSTAYMQLSLTSEDSAVYYCARYDYGGSYFDYWGQGTTLTVSS 120

RESULT 14
O924R2 PRELIMINARY; PRT; 140 AA.
AC -O924R2:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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```
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067788; BAB63273.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 140
FT NON_TER 140
FT NON_TER 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match
Best Local Similarity 73.3%; Score 454; DB 11; Length 140;
Matches 84; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Oy 1 EVOLQSQPELVKPGKTSVRISCKTSGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGTTY 60
Db 1 QVQLQQPQGAELVKGASVKLSCKASGYTFTSYWMHWKQRPGRGLEWIGRIDPNSSGGTKY 60

Oy 61 NOKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAGWNFDYWGQGTTLTVSS 115
Db 61 NEKFKRATLTVDKPSSTAYMQLSLTSEDSAVYYCARIYAGDIWGQGTSTVTVSS 115

RESULT 15
O924P5 PRELIMINARY; PRT; 144 AA.
AC -O924P5:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069920; BAB63936.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 144
FT NON_TER 144
FT NON_TER 144
SQ SEQUENCE 144 AA; 15865 MW; CD07BE97E95C1B27 CRC64;

Query Match
Best Local Similarity 73.2%; Score 453; DB 11; Length 144;
Matches 85; Conservative 12; Mismatches 18; Indels 4; Gaps 1;

Oy 1 EVOLQSQPELVKPGKTSVRISCKTSGYTFTEYTHHWKQSHGKSLSEWIGNINPNNGGTTY 60
Db 1 QVQLQQPQGAELVKGASVKLSCKASGYTFTSYWMHWKQRPGRGLEWIGRIDPNSSGGTKY 60

Oy 61 NOKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCA----AGNFDYWGQGTTLTVSS 115
Db 61 NEKFKRATLTVDKPSSTAYMQLSLTSEDSAVYYCASYGSSYWFYDWGIGTGTTVTVSS 119

Search completed: July 21, 2003, 13:35:07
Job time : 51.7658 secs
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